

# STIC Search Report Biotech-Chem Library

### STIC Database Tracking Number

TO: Nancy Vogel

Location: rem/2a70/2c70

Art Unit: 1636

Wednesday, May 11, 2005

Case Serial Number: 09/896888

From: Edward Hart

**Location: Biotech-Chem Library** 

**REM-1A55** 

Phone: 571-272-2512

edward.hart@uspto.gov

#### Search Notes

Examiner Vogel,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

**Edward Hart** 



Ins pole Blonk Usolo)

#### STIC-Biotech/ChemLib

From:

Vogel, Nancy

Sent:

Tuesday, May 03, 2005 7:14 AM

To:

STIC-Biotech/ChemLib

Subject:

sequence search for 09/896,888

please do sequence search of SEQ ID NO:1, nucleotides 351-527 of SEQ ID NO:1, and SEQ ID NO:10, including interference files,

of 09/896,888

and return results to me on paper asap.

Thanks

Nancy Vogel Patent Examiner Art Unit 1636 Office: Remson 2A70 Mail Box: Remson 2C70 (571) 272-0780

STAFF USE ONLY

Searcher:\_

Searcher Phone: 2-

Date Searcher Picked up

Date Completed:\_\_\_

Searcher Prep/Rev. Time

Online Time:\_

Type of Search

Interference:\_

SPDI:

Oligomer:\_ Encode/Transl:

Structure#:\_

Inventor:\_\_\_\_ Litigation:\_\_\_

\*\*\*\*\*\*\*\* Vendors and cost where applicable

STN:\_ DIALOG:

QUESTEL/ORBIT:

LEXIS/NEXIS:\_

SEQUENCE SYSTEM:

WWW/Internet:\_

Other(Specify):\_

mis page Bank lusbo)



### STIC SEARCH RESULTS

### Biotech-Chem Library

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor Remsen Bldg. 01 D86 571-272-2507

### Voluntary Results Feedback Form

>	I am an examiner in Workgroup: Example: 1610
>	Relevant prior art found, search results used as follows:
	☐ 102 rejection
	☐ 103 rejection
	☐ Cited as being of interest.
	Helped examiner better understand the invention.
	☐ Helped examiner better understand the state of the art in their technology.
	Types of relevant prior art found:
	☐ Foreign Patent(s)
	Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)
>	Relevant prior art not found:
	Results verified the lack of relevant prior art (helped determine patentability).
	☐ Results were not useful in determining patentability or understanding the invention.
Co	mments:

Prepolitorendecompleted forms to STIC Blotch Chem Library Remem Blog



Inis pose Blonk Usolo)

"IND TUSE BIOTIK (USDIO)

nucleic

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Run on:

Sequence:

Searched:

Database

Result No.

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158575 Sequence 41
16,1307 Sequence 11
AX233349 Sequence 12
AX353349 Sequence CQ504346 Sequence AX361570 Lac promote BD175852 A method AX404725 Sequence 1 192481 Sequence 2 G02286 human STS SCQ506464 Sequence AJ535749 Cicer ari M10349 Cloning vec M12465 Sequence AJ535745 Sequence AJ535745 Sequence AJ535745 Cicer ari M10349 Cloning vec M13485 Sequence AJ535745 Sequence AJ535745 Sequence AJ535745 Sequence
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unclassified.
1 (bases 1 to 50)
Grigliatti,T.A., Theilmann,D.A., Pfeifer,T.A. and Hegedus,D.D.
Grigliatti,T.A., Theilmann,D.A., Pfeifer,T.A. and Hegedus,D.D.
Theether expression vectors
Patent: JP 200151625-A 13 25-SEP-2001;
THE UNIVERSITY OF BRITISH COLUMBIA
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PD 25-SEP-201
PF 26-MAR-1998 JP 1998541010
PR 27-MAR-1997 US 60/049946,28-JAN-1998 CA
THOMAS A GRIGIATTI, DAVE A THEILMANN, THOWAS
A PFEIFER, DWAYNE D
PI HEGEDUS
PC C12N15/85,C12N5/06,C12N15/69//C12N9/22
CC Insect expression vectors
FH Key Location/Qualifiers
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    /organism="unidentified"
/mol_type="genomic DNA"
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AC015852 Homo sapi
AC013998 Homo sapi
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Gaps

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f 100 bp

g of 800 bp in length

g of 808 bp in length

f 100 bp

g of 802 bp in length

g of 802 bp in length

g of 751 bp in length

f 100 bp in length

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HOMO sapiens (human)

Elkaryota; Metaza; Chordata; Craniata; Vertebrata; Euteleostomi;

Butaryota; Metaza; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 99591)

S Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 2, clone RP11-429N24

Thomblished

Elitton, E., Linton, L., Bouhdalter, B., Barren, B., Linton, L., Bouhdalter, B., Barren, B., Linton, L., Bouslavity, L., Bouhdalter, B., Barren, B., Linton, L., Bouhdalter, B., Barren, B., Linton, L., Dowar, K., Domaino, M., Donelan, L., Doyle, M., Cooke, P., DeArellano, K., Dowar, K., Domaino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, M., Grartes, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lieu, C., Locke, K., McCandald, P., Marquis, N., McBurn, P., McGurk, A., McKernan, K., McCandald, P., Marquis, N., Peterson, K., Pollara, V., Riley, R., Santos, R., Santos, S., Santos, S., Santos, S., Santos, S., Santos, S., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Ray, Wann, D., Ye, W.J., Zimmer, A. and Zody, M., Santos, S., Wu, X., Myman, D., Ye, W.J., Zimmer, A. and Zody, M.

Lustel, 3000 this sequence version replaced gi:6425709.

All repeats were identified using RepeatMasker. html

Center: Whitehead Institute/ MIT Center for Genome Center

Center: Whitehead Institute/ MIT Center for Genome Center
                                                           99591 bp DNA linear HTG 13-JUL-2000
Homo sapiens chromosome 2 clone RP11-429N24 map 2, LOW-PASS
SEQUENCE SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  * NOTE: This record contains 111 individual
* sequencing reads that have not been assembled into
* contigg. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
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Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
Conter: project Information
Center project name: L3805
Center clone name: 429_N_24
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Sirren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, J., Castle, A., Collangelo, M., Collangelo, M., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, M., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Mordons, B., Hagos, B., Heaford, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McKernan, K., Mcdanghlin, J., Melfrim, J., Melfrim, J., Merkernan, K., Mchaughlin, J., Melfrim, J., Peterson, K., Pollara, V., Riley, R., Surangalin, J., Surangan, C. H., O'Connor, T., O'Donnell, P., Strage-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M. Christ for Genome Charles and Control of the American Collaboration of the American Collaboration of the American Collaboration of the Ameri
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Direct Submission

Submitted (66-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

123 (bases 1 to 118229)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Anderson, S., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearrellano, K., Dewar, K., Daz, J.S., Collymore, A., Cooke, P., Dearreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Karatas, A., Klein, J., Lakcoque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McDwan, P., McGurk, A., McKernan, K., McPheeters, R., McGarth, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Macdonald, P., Marquis, N., Waylor, J., Norman, C.H., O'Connor, T., O'Connell, P., O'Neil, D., Olivar, T.M., Norman, C.H., O'Connor, T., O'Connell, P., Pisani, C., Pollara, Y., Raymond, C., Riley, R., Rogov, P., Rothman, D., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Taragilio, J., Vonsiller, W., Wilson, B., Wu, X., Wyman, D., Ye, Wol, Stonon, C., Milson, B., Wu, X., Wyman, D., Ye, Wol, Stonon, C., Milson, B., Wu, X., Wyman, D., Ye, Wol, Stonon, C., Simer, A., Anderson, M., Taragilio, J., Vonsiller, A., Allen, A.,
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                         Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 22, clone RP11-348B6 Unpublished
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Web site: http://www-seq.wi.mit.edu
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                    AC013315.3 GI:912390
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> HTG 24-AUG-2002 LOW-PASS

AC013315 118229 bp DNA linear Homo sapiens chromosome 22 clone RP11-348B6 map 22, SEQUENCE SAMPLING.

DEFINITION

RESULT 3 AC013315

8 3

3876 TTAATTGCGTGGCGCTGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 3923

3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG

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overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.
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Homo sapiens clone RP11-11016, LOW-PASS SEQUENCE SAMPLING.
AC013368.6 GI:9123839
HTGS - HTGS - PHASE0.
HOMO sapiens (human)
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 211967)
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3 of 865 bp in length
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                                                         Strong-Linton, L. Musbaum, C., Lander, E., Allen, N., Anderson, M., Birren, B., Linton, L., Musbaum, C., Lander, E., Allen, N., Anderson, M., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Costellan, C., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Merldrim, J., Merwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Merwan, D., McGurk, A., Morkenan, K., McLaughlin, J., Meldrim, J., Peterson, K., Pollara, V., Riley, R., Say, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M., Wheeler, J., Wu, X., Wuman, D., Ye, W. J., Zimmer, A. and Zody, M. and Zody, 
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* sequencing reads that have not been assembled into
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* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
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Birren, B., Linton, L., Nusbaum, C. and Lander, B.
Homo sapiens, clone RP11-11016
Unpublished
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Donelan, L., Doyle, M.,

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Seearch, 320 Charles Street, Cambridge, Ma V2111, USA

Research, 320 Charles Street, Cambridge, Ma V2111, USA

S Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F.,
Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G.,
Campoplano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,
Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,
Dodge, S., Domino, M., Doyle, M., Ferreitz, P., FitzHugh, W., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Grahm, L.,
Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., LaRocque, K., Lamazres, R., Landers, T., Lehoczky, J.,
Klein, J., LaRocque, K., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
McCarthy, W., McEwan, P., McGurk, A., McKernan, K., McThecters, N.,
Minoy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,
O'Neil, D., Olivar, T., Minova, T., Miranda, C., Mlenga, V., Morrow, J.,
Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
Young, G., Zainoun, J., Zimmer, A. and Zody, M., Trigilio, J.,
Voung, G., Zainoun, J., Zimmer, A. and Zody, M. Trigilio, J.,
Direct Submission

AL Submisted (Ja-Aug-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
          Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Perreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Gadagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J. C., Johnson, R., Jones, C., Kamn, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGwan, P., McKernan, K., McLaughlin, J., Meldrim, J., Peterson, K., Pollara, V., Riley, R., So, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M., Wheeler, J., Wu, X., Direct Submission
                                                                                                                                                                                                                                                   Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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* sequencing reads that have not been assembled into
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* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
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Web site: http://www-seq.wi.mit.edu
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HOMO sapiens chromosome 18 clone CTB-155C15 map 18, LOW-PASS
SEQUENCE SAMPLING.
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,J., Barna,N., Beckerly,R., Boguslavkiy,L., Boukhgalter,B.,
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AUTHORS
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KEYWORDS
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AC015852
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cont.g of 100 bp
contig of 876 bp in length
gap of 100 bp
contig of 892 bp in length
gap of 100 bp
contig of 889 bp in length
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4: contig of 877 bp in length
4: gap of 100 bp
5: contig of 880 bp in length
6: gap of 100 bp
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9: contig of 886 bp in length

9: gap of 100 bp

9: contig of 881 bp in length

9: gap of 100 bp
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5: contig of 871 bp in length

1: gap of 100 bp

1: contig of 880 bp in length

2: gap of 100 bp
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contig of 872 bp in length
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contig of 867 bp in length
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Homo sapiens clone 1_E_17, LOW-PASS SEQUENCE SAMPLING.
AC010800
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 0.0032;
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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School-Month, N. 18. Colaboric N. Subtraents R. Severy, P. Verface, S. Tirrell, A. Vessiliev, R. Subtraents A. A. Tirrell, A. Vessiliev, R. Subtraents A. A. Wheeler, J. Wux. Y. Wand. D. Colaboric Colaboric State Colaboric Co										- 2										-															
	Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfarye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.	omitted (23-5EP-1999) Whitehead institute/MIT Center for Genome search, 320 Charles Street, Cambridge, MA 02141, USA largeats were identified using RepeatMasker: Smit, A.F.A. & een. P. (1966-1997)	p://ftp.genome.washington.edu/RM/RepeatMasker.html. NOTE: This record contains 86 individual sequencing reads that have not been assembled into	contigs. Runs of N are used to separate the reads and the order in which they appear is completely continued to the contract of the contract o	aidliary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows yverlab relationships among clones to be deduced.	However, it should not be assumed that this clone will be sequenced to completion. In the event that that the record is undated, the accession number will	be preserved.	gap of unknown le	1695: contig of 836 bp in gap of unknown lengt	2546: contig of 851 bp in	3398: contig of 852 b	gap or unknown 4263: contig of 865 by	gap of unknown lengt 5163: contig of 900 bp in	gap of unknown le 6030: contig of 867 bp	gap of unknown le	gap of unknown lengt 7717: contid of 816 bp in	gap of unknown le	gap of unknown le	9412: contig of 847 bp gap of unknown le	10266: contig	11243: contig of	12098: contig of	gap or 12940: contig	gap of 13799: contig	gap of 14670: contig	gap ot 15489: contig	gap of 16379: contig	gap of 17216: contig	gap of 18204: contig	gap of 19021: contig	gap of	gap of 20718: contid	gap of unknow 21555: contiq of 837	gap of	gap of

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I. Chases I to 217141)

Signature and the control of 
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Homo sapiens clone RP11-337M23, LOW-PASS SEQUENCE SAMPLING.
ACO73998
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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contig of 856 bp in length
gap of unknown length
contig of 820 bp in length
gap of unknown length
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gap of unknown length
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of 832 bp in length
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone RP11-337M23
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Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theedore, J., Tirrell, A., Travers, M., Trigilio, J., Vasiliev, H., Viel, R., Milson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission
Submitted (19-JUL-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 30, 2000 this sequence version replaced gi:9838018.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washingcon.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                         ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * NOTE: This record contains 270 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
Center project name: L7934
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(Spriniformes; Cyprinidae; Danio.

(Barinda,N., Knapik,E.W., Ziniti,J., Sim,C., Yamada,E., Kaplan,S., Jackson,D., de Sauvage,F., Jacob,H. and Fishman,M.C.

Cebrafish genetic map with 2000 microsatellite markers

Genomics 58 (3), 219-232 (1999)
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Massachusetts General Hospital
Mail code 1494100A, 149 13th Street, Charlestown, MA 02129, USA
Fax: 617726580
Email: fishman@mgh.cvrc.harvard.edu
http://zebrafish.mgh.harvard.edu
primer A: CACCGACCTTCACTGACGTA
Primer B: ATACACCCCAAGCCGACAT
STS size: 112
PCR Profile:
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Pred. No. 0.0054;
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AUTHORS
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C12P21/02/C12Q1/02,
PC C12Q1/68,G01N33/15,G01N33/50,G01N33/56,G01N33/68,
PC C12N15/00,
PC C1 PQUALB A, L, G, Or C
PC C1 PQUALB A, L, G, Or C
PC C2 PQUALB A, L, G, Or C
PC C3 PQUALB A, L, G, Or C
PC C4 PQUALB A, L, G, Or C
PC C6 PQUALB A, L, G, Or C
PC C7 PQUALB A, L, G, Or C
PC C7 PQUALB A, L, G, Or C
PC PQUALB A, L, G, Or C
PQUALB A, L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          826 bp DNA linear STS 01-FEB-2001 rerio STS genomic, sequence tagged site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 826)
Shimoda,N., Knapik,B.W., Ziniti,J., Sim,C., Yamada,B., Kaplan,S., Jackson,D., de Sauvage,F., Jacob,H. and Fishman,M.C.
Schrafish genetic map with 2000 microsatellite markers
Genomics 58 (3), 219-232 (1999)
                                                                                                                                             AGIP21/04,

AGIP25/00, AGIP25/14, AGIP25/16, AGIP25/28, AGIP25/30, AGIP27/02,

AGIP27/00, AGIP29/00, AGIP31/04, AGIP31/10, AGIP31/12, AGIP31/18,

AGIP33/00,

AGIP33/00,

AGIP33/00,

AGIP33/00,

CO7K14/47, CO7K16/18, CI2N1/15, CI2N1/19, CI2N1/21, CI2N5/10 PC
                                                          PC A61P9/06,A61P9/08,A61P9/10,A61P9/12,A61P9/14,A61P11/00 PC
,A61P11/06,A61P13/02,
PC A61P13/12,A61P15/00,A61P17/02,A61P17/06,A61P19/02,A61P21/00,
        A61P1/16, A61P3/10, A61PS/00, A61P7/02, A61P7/04, A61P7/06, A61P7/08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cardiovascular Research Center
Massachusetts General Hospital
Mail code 1494100A, 149 13th Street, Charlestown, MA 02129, USA
Fax: 6177265806
Email: fishmandmgh.cvrc.harvard.edu
http://zebrafish.mgh.harvard.edu
primer A: CACATGTGGACCGGACTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism='Homo sapiens (human)'.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        168 TTAATNGCGTTGCGCTCACTGCCGGCTTTCCAGTCGGGAAACCTGTCG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
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8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71.6%; Score 35.8; DB 6 83.3%; Pred. No. 0.0067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .745
/organism="Homo
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27956 Zebrafish AB Danio
G40613
G40613.1 GI:3359822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Danio rerio (zebrafish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 83.3
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Danio rerio
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                                      A61P9/
                                                                                                                        Query Match
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G40613
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AUTHORS
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anotes—Yorcors. milMP19 with added BstXI site; V-type: Phage; Genomic DNA from a single adult Zebrafish of AB strain was digested with Alu1, Cac81, HaelII, NlaVI, or RsaI. Fragments in the range of 250-500 bp were gal purified and a BstXI linker was added. The fragments were closed into a modified Milamp19 vector and transformed into B. COll pHSalpha. Microsatelllite sequences were screened with labeled d(CA)15 and d(GT)15 oligonucleotide
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CRAIG A ROSEN, STEVEN M RUBEN, REINHARD EBNER, PAUL E YOUNG, JIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PI PAUL A MOORE, GEORGE KOMATSOULIS, CHARLES E BIRSE PC C12N15/09, A61K31/7115, A61K35/76, A61K38/00, A61K45/00, A61K48/00, PC PC PC
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1 (bases 1 to 745)
Rosen,C.A., Ruben,S.M., Ebner,R., Young,P.E., Ni,J., Moore,P.A., Komatsoulis,G. and Birse,C.E.

33 human secreted proteins
Patent: JP 2002534972-A 36 22-0CT-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.6%; Score 35.8; DB 11; Length 604; ilarity 83.3%; Pred. No. 0.0067; Conservative 0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            562
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                                                                                                                                                                                                                                                                                     Primers are available from Research Genetics Inc.
                                                                                                                                                                                                                                                                                                            (http://www.resgen.com phone: 800-533-4363)
    Location/Qualifiers
                                                                                                                                          1.5 mM
50 mM
10 mM
8.3
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each 200 uM
0.034 units/ul
10 ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Zebrafish AB"
/dev_stage="Adult"
/lab_host="DH5alphaF'IQ"
                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="AB"
                                                                                                                                                                                                                                                                                                                                                                                                     'organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          745 bp
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19-JAN-1999 US 60/1163:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188. .207
complement (280. .299)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33 human secreted proteins.
BD269301
                                                                                                                                                                  KCl:
Tris-HCl:
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OS Homo sapiens (human)
PN JP 2002534972-A/36
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JP 2002534972-A/36.
Homo sapiens (human)
                                                                                                                                             MgCL2:
dNTPs:
Taq Polymerase:
Total Vol:
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Best Local Similarity
Matches 40; Conserv
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                                                                                                                Buffer:
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ORIGIN
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SOURCE
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AUTHORS
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JOURNAL
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Gaps

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/dev_stage="Adult"

| Jab host="DH5alphaF'IQ"
| Anote="Vector: ml3MH19" with added BstXI site; V-type: Phage; Genomic DNA from a single adult Zebrafish of AB strain was digested with Alu1, Cac81, HaeIII, NlaVI, or RasI. Fragments in the range of 250-500 bp were gel, purified and a BstXI linker was added. The fragments were cloned into a modified Mi3mp19 vector and transformed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               into E. Coli DH5alpha. Microsatelllite sequences were screened with labeled d(CA)15 and d(GT)15 oligonucleotide
                                                                                          Contact: Mark C. Fishman
Cardiovascular Research Center
Massachusetts General Hospital
Mail code 1494100A, 149 13th Street, Charlestown, MA 02129, USA
Fax: 6177265806
Zebrafish genetic map with 2000 microsatellite markers
Genomics 58 (3), 219-232 (1999)
99303552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 11; Length 979;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
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                                                                                                                                                                                                                                                                                                                      94 degrees C for 5.0 minutes 94 degrees C for 1.0 minute 58 degrees C for 1.0 minute 72 degrees C for 1.5 minute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     are available from Research Genetics Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phone: 800-533-4363)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.5 mM
50 mM
10 mM
8.3
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Pred. No. 0.0068;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                       MJ Research PTC-100
                                                                                                                                                                                                Email: fishman@mgh.cvrc.harvard.edu
http://zebrafish.mgh.harvard.edu
Primer A: TCAATCTGAAACTCGGA
Primer B: CGCTTTATAGGGCTGCAGG
STS size: 244
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.034 units/ul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone lib="Zebrafish AB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              each 375 nM
each 200 uM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Danio rerio"
/mol type="genomic DNA"
/strain="AB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db xref="taxon:7955"
/map="LG 16"
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complement (344. .363)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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Tris-HCl:
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83.3%;
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PCR Cycles: 2
Thermal Cycler: M
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                                                                                                                                                                                                                                                                                                                                              Denaturation:
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                                                                                                                                                                                                                                                                                                                                                               Annealing:
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Primer:
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Best Local Similarity
Matches 40; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Protocol:
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primer_bind
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PUBMED
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                                                                                COMMENT
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/dev stage="Adult"
/dev stage="Adult"
/lab_nost="DHSalphar'IQ"
/hab_nost="DHSalphar'IQ"
/note="Vector: mi3Mp19 with added BstXI site; V-type:
Phage; Genomic DNA from a single adult Zebrafish of AB
strain was digested with Alu!, Cac81, HasII, NINIV, or
RsaI. Fragments in the range of 250-500 bp were gel
purified and a BstX1 linker was added. The fragments were
cloned into a modified Mi3mp19 vector and transformed
into B. COli MBSalpha. Microsatelllite sequences were
screened with labeled d(CA)15 and d(GT)15 oligonucleotide
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220177 Zebrafish AB Danio rerio STS genomic, sequence tagged site.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Ostariophysi,
Cypriniformes, Cyprinidae, Danio.

(Cypriniformes, Cyprinidae, Danio.

(Dases 1 to 979)
Shimoda,N., Knapik,E.W., Ziniti,J., Sim,C., Yamada,E., Kaplan,S.,
Jackson,D., de Sauvage,F., Jacob,H. and Fishman,M.C.
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71.6%; Score 35.8; DB 11; Length 826;
Best Local Similarity 83.3%; Pred. No. 0.0068;
Matches 40; Conservative 0; Mismatches 8; Indels 0;
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                                                           94 degrees C for 5.0 minutes 94 degrees C for 1.0 minute 58 degrees C for 1.0 minute 72 degrees C for 1.5 minute
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Location/Qualifiers
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10 mM
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each 375 nM
each 200 uM
0.034 units/ul
10 ul
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'strain="AB"
  Primer B: TCTCTCCCCTGGACATCATC
STS size: 142
PCR Profile:
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/map="LG 16"
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!: contig of 773 by ....
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S Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, M., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Farestor, J., Berreira, P., Fitzhugh, W., Forrest, C., Gage, D., Glandero, S., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Howland, J.C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Largocque, K., Lehocaky, J., Levine, R., McKernan, K., McHoes, K., McCarth, M., McMenan, D., McGaurk, A., McKernan, K., McHoesers, R., Medirim, J., Mencus, L., Minova, T., Miranda, C., Manga, V., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Fley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Subramanian, A., Talamas, J., Tarell, A., Traers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A. and
ACUZ3542 76295 bp DNA linear HTG 13-JUL-2000 SEQUENCE SAMPLING.
                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 76295)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 15, clone RP11-165P21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission.
Submitted (15-FBB-2000) Whitehead Institute/MIT Center for Genome Submitted (15-FBB-2000) Whitehead Institute/MIT Center for Genome Steesarch, 320 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this sequence version replaced gi:6978228.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * NOTE: This record contains 86 individual
sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
rarbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
However, it should not be assumed that this clone
will be sequenced to completion. In the event that
the record is updated, the accession number will
be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center: Whitehead Institute/ MIT Center for Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
_------ Project_Information
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Center clone name: 165_P_21
                                                                            AC023542.2 GI:9156023
HTG; HTGS PHASE0.
Homo sapiens (human)
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S (bases I to 75002)

S Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barnan, N., Bada, F., Boguslavkiy, L., Anderson, S., Baldwin, J., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dedare, K., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Firzhugh, W., Forrest, C., Gage, D., Fenestor, J., Ferreira, P., Firzhugh, W., Forrest, C., Gage, D., Grand-Pierre, N., Grand-Pierre, N., Grand, P., Horlon, L., Karatas, A., Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kam, L., Karatas, A., Klein, J., Largocque, K., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McGark, A., McKernan, K., McDarteres, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Menga, V., Morrow, J., Naylor, J., Norman, C. H., O'Comnor, T., O'Donnell, P., O'Nell, D., Olivar, T. M., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubraanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Young, G., Zainoun, J., Zimmer, A. and, Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 75002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (14-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this sequence version replaced gi:6970532.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                    ACUZ3384 75002 bp DNA linear HTG 13-JUI
Homo sapiens chromosome 11 clone RP11-589112 map 11, LOW-PASS
SEQUENCE SAMPLING.
                                                               compositions, kits, and method for identification
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                                                                            assessment, prevention, and therapy of ovarian cancer Patent: WO 0170979-A 13142 27-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                           DB 6; Length 586;
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Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                          Score 35.6; DB 6
Pred. No. 0.008;
0; Mismatches
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/mol_type="unassigned DNA"
/db xref="taxon:9606"
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Homo sapiens (human)
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82.0%;
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Matches 40; Conservative
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DEFINITION

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ACCESSION VERSION KEYWORDS

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SOURCE

\* NOTE: This record contains 88 individual

\* sequencing reads that have not been assembled into

\* contigs. Runs of N are used to separate the reads

\* and the order in which they appear is completely

\* arbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows

\* overlap relationships among clones to be deduced.

\* However, it should not be assumed that this clone

\* will be sequenced to completion. In the event that

\* the record is updated, the accession number will

\* be preserved. Contact: sequence\_submissions@genome.wi.mit.edu ------- Project Information ------ project name: 1.5114 Center project name: 589\_1.12 contig contig contig and so that is contig of 751 bp in length contig of 751 bp in length contig of 754 bp in length gap of 100 bp contig of 754 bp in length gap of 100 bp contig of 746 bp in length gap of 100 bp contig of 764 bp in length gap of 100 bp contig of 760 bp in length gap of 100 bp contig of 772 bp in length gap of 100 bp contig of 762 bp in length gap of 100 bp contig of 762 bp in length gap of 100 bp contig of 762 bp in length gap of 100 bp contig of 741 bp in length gap of 100 bp contig of 739 bp in length gap of 100 bp contig of 749 bp in length gap of 100 bp 100 bp of 755 bp in length 100 bp of 754 bp in length gap of 100 bp contig of 782 bp in length gap of 100 bn gap of 100 bp contig of 732 bp in length gap of 100 bp contig of 784 bp in length gap of 100 bp contig of 749 bp in length gap of 100 bp contig of 739 bp in length 100 bp of 752 bp in length gap of 100 bp contig of 751 bp in length bp in length bp in length bp in length contig of 724 bp in length gap of 100 bp 100 bp of 743 bp in length gap of 100 bp contig of 743 bp in length 100 bp of 738 bp in length gap of 100 bp contig of 751 bp in length 774 bp in length contig of gap of 100 contig of gap of 100 contig of contig d contig contig qap of gap of gap of gap of gap of 23926: 24674: 1673: 2455: 2555: 11078 14492 18615 7655 8409 8409 9255 10125 110219 11051 111951 11355 11 20345 20445 21206 21306 22090 22973 23827 23827

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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 95127)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens, clone RP11-1015

Unpublished
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Center: Whitehead Institute/ MIT Center for Genome Research
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Homo sapiens clone RP11-1J15, LOW-PASS SEQUENCE SAMPLING.
AC016798
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* sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
arbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
However, it should not be assumed that this clone
will be sequenced to completion. In the event that
the record is updated, the accession number will
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------ Project Information
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ö Gaps 20592 AITIAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 20641 ö Query Match 71.2%; Score 35.6; DB 2; Length 95127; Best Local Similarity 82.0%; Pred. No. 0.0091; Matches 41; Conservative 0; Mismatches 9; Indels 0; 20 1 ACTTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG a

Search completed: May 10, 2005, 05:52:47 Job time : 306.908 secs

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SUMMARIES

	Description	Aav62498 Plasmid p	Aas89978 DNA encod	Aas92596 DNA encod	Aaa87692 Human sec	Acn86091 Breast ca	Acn83021 Breast ca	Aaf55360 Sequence	Adl39252 Human ova	Aas77556 DNA encod	Aas77545 DNA encod	Aas69138 DNA encod	Aas77547 DNA encod	Aas87523 DNA encod	Aas77561 DNA encod	Ade09733 Novel DNA	Aas69873 DNA encod	Ade48102 Human che	Aas69432 DNA encod	Aas85906 DNA encod	Aas92595 DNA encod
	ID	AAV62498	AAS89978	AAS92596	AAA87692	ACN86091	ACN83021	AAF55360	ADL39252	AAS77556	AAS77545	AAS69138	AAS77547	AAS87523	AAS77561	ADE09733	AAS69873	ADE48102	AAS69432	AAS85906	AAS92595
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### ALIGNMENTS

RESULT 1 AAV62498

Op ie2; promoter; shuttle vector; transformation; melanotransferrin; immediate early baculovirus promoter; prokaryotic; transcription; bleomycin/phleomycin-type antibiotic; insect cell; transposon; ion transport peptide hormone; PCR primer; ss. Plasmid p2ZOp2J-3 constructing primer 2. BP. UYBR-) UNIV BRITISH COLUMBIA. 97US-0049946P. 98CA-02221819. 98WO-CA000282. AAV62498 standard; DNA; 50 (first entry) WO9844141-A2 26-MAR-1998; 27-MAR-1997; 28-JAN-1998; 19-JAN-1999 08-OCT-1998 Synthetic. AAV62498; 

Hegedus DD; Pfeifer TA, Theilmann DA, Grigliatti TA,

Expression vectors for transforming insect cells from disparate lines useful to express heterologous DNA, e.g. to allow study of gene expression and produce commercially important proteins. WPI; 1998-557129/47.

Disclosure; Page 39; 121pp; English.

Primers AAV62497 and AAV62498 were used for the construction of the plasmid p2Z0p37-3. The invention provides a new shuttle vector for transforming insect cells that comprises: (i) prokaryotic origin of replication; (ii) insect promoter having homology to, and capable of functioning as, an immediate early baculovirus promoter; (iii)

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            conferring resistance to a becay claim, and the section market capable of conferring resistance to a becay claim, in insect and prokaryotic transcriptional control of (ii) and (iii), in insect and prokaryotic cells respectively. The vectors can be used to stably transform (especially insect) cells with heterologous DNA, is useful to allow study of gene expression and direct expression of heterologous gene products, such as commercially important proteins. They are especially useful to allow expression of melanotransferrins, ion transport peptide hormones or biologically active derivatives in insect cells. They enable transformation of insect cell in insect cells. They enable screening of lines for optimum post-translational modification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnospitics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is
                                                                                                                                                                                                                        particular proteins. Shuttle vectors further comprising DNA transposable elements defining a transposon can be used to optimise heterologous
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prokaryotic promoter sequence, and (iv) selectable marker capable of
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23-AUG-2000; 2000US-00649167.
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supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder, ss.
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                                                                                                                                                                                                                                                                        Sequence 16091 BP; 4724 A; 3867 C; 3861 G; 3639 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                 Length 16091;
                                                                                                                                                                                                                                                                                                                                                                                                                       8080 GITIATIGCAATCATIGCCCGCTTTCCAGTCGGGAAACCTGTCG 8037
                                                                                                                                                                                                                                                                                                                                                       5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                  7 GCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding novel human diagnostic protein #28400.
                                                                                                                                                                                                                                                                                                               72.0%; Score 36; DB 5; 88.6%; Pred. No. 0.00011;
                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 28400; 103pp; English.
                                                                                                                                                                                                            electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAS92596 standard; cDNA; 20795 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 88.6
Matches 39, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-639362/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; ABG28409.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS92596;
                                                                                                                                                                                                                                                                                                                   Query Match
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involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in ftp.wipo.int/pub/published_pct_sequences
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Sequence 20795 BP; 4255 A; 5208 C; 5716 G; 5614 T; 0 U; 2 Other;

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                              Gaps
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72.0%; Score 36; DB 5; Length 20795; 88.6%; Pred. No. 0.00011;
          0.00011;
ches 5; Indels
                                                          20
                                                         7 GCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
                            0; Mismatches
            Local Similarity 88.6
nes 39, Conservative
 Query Match
                            Matches
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12363 GITTATTGCAATCATTGCCCGCTTTCCAGTCGGGAAACCTGTCG 12406

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## AAA87692 standard; cDNA; 745 BP AAA87692;

04-DEC-2000 (first entry)

Human secreted protein gene 27 SEQ ID NO:37.

Human; secreted protein; immunosuppressive; immunostimulant; nootropic; antiinfemmatory; cardiant; vulnerary; antiulcer; anticonvulsant; antiparkinsonian; neuroprotective; antivoral; antibacterial; cytostatic; antiparasitic; thrombolytic; anticoagulant; antiarteriosclerotic; antiparasitic; thrombolytic; anticoagulant; antiarteriosclerotic; cancer; immune system disorder; hyperproliferative disorder; infection; cardiovascular disorder; hyperproliferative disorder; infection; cardiovascular disorder; neurological disease; wound healing; ss.

Homo sapiens

WO200043495-A2

27-JUL-2000

18-JAN-2000; 2000WO-US000903

99US-0116330P 19-JAN-1999; (HUMA-) HUMAN GENOME SCI INC

Moore PA; ۵, Z, Young PE, Ebner R, CE; Ruben SM, Komatsoulis G, Rosen CA,

2000-499225/44. P-PSDB; AAB25691. New isolated polynucleotide encoding a secreted protein useful for preventing, treating or ameliorating a medical condition.

Claim 1; Page 394; 451pp; English.

expressed in. Examples of activities include: immunosuppressive; immunostimulant; antiinflammatory; cardiant; vulnerary; antiulcer; notropic; antiviral; anticonvulsant; antiparkinsonian; neuroprotective; antibacterial; antiparasitic; thrombolytic; anticoagulant; antiarteriosclerotic and cytostatic. The secreted proteins and their polynucleotides can be used in gene therapy and as vaccines, chemotaxismodulators and angiogenesis- modulators. The human secreted proteins and The polynucleotide sequences given in AAA87666 to AAA87708 encodes the human secreted proteins given in AAB25665 to AAB25755. Human secreted proteins have activities based on the tissues and cells the genes are

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                                                                                                                                         infection. AAA87657 to AAA87665 and AAB25664 represent sequences
                pathological condition by determining the presence or absence of a mutation in the polynucleotide or determining the presence or amount of expression of the protein. The polynucleotides and proteins can also be used in the treatment and diagnosis of cancer, diseases of the immune system, hyperproliferative disorders, cardiovascular disorders and neurological disease. They can also be used to promote wound healing and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
polynucleotides can be used for diagnosing (the susceptibility to) a
                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated polypeptide associated with breast cancer, useful for detecting presence of polypeptide in sample, as a marker for breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.
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                                                                                                                                                                                                                                                                                                                                                            168 rraarngcgrrdcgcrcacrdcccccrrrccagrcdggaaaccrdrcg 121
                                                                                                                                                                                                                                                                                                                         20
                                                                                                                                                                                                                                       Score 35.8; DB 3; Length 745; Pred. No. 5.9e-05; 0; Mismatches 8; Indels
                                                                                                                                                                                                    Sequence 745 BP; 191 A; 214 C; 188 G; 142 T; 0 U; 10 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 791 BP; 188 A; 198 C; 211 G; 182 T; 0 U; 12 Other;
                                                                                                                                                                                                                                                                                                                         3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
                                                                                                                                                          used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Breast cancer related marker, seg id 7241.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, SEQ ID NO 7241; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y, Steinmann K;
                                                                                                                                                                                                                                         71.6%;
83.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MILL-) MILLENNIUM PHARM INC.
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83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACN86091 standard; DNA; 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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Best Local Similarity 83.3
Matches 40; Conservative
                                                                                                                                                                                                                                                                                 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang
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                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Χu Υ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US2003099974-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACN86091;
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated polypeptide (I) associated with breast cancer which is encoded by a nucleic acid molecule comprising a nucleotide sequence (SI). Further disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the invention may be described as cytostatic. The antibody is useful for detecting the presence of (I) in a semple. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (I) is useful as a marker for breast cancer and in breast cancer therapy. Sequences given in records ACN7851-ACN92934 represent nucleic acid markers associated with breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPTO web
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence obtained after sequencing with modified Taq DNA polymerase.
                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated polypeptide associated with breast cancer, useful for detecting presence of polypeptide in sample, as a marker for breast
                                                                                                                                                                                 Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.
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Pred. No. 6.1e-05;
0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     569 Traarrecerrececrnacrececrrrecagressaaacereres 616
                                544 Traarrgcgingcgcrcacrcccccrrrccagicgggaaccrgrcg 591
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           20
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           TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      site at segdata.uspto.gov/sequence.html?DocID=20030099974
                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 4171; 36pp; English.
                                                                                                                                                            Breast cancer related marker, seq id 4171
                                                                                                                                                                                                                                                                                                                                              Wang Y, Steinmann K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF55360 standard; DNA; 327 BP
                                                                                         BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 71.6%;
1 Similarity 83.3%;
40; Conservative (
                                                                                                                                                                                                                                                                           18-JUL-2002; 2002US-00198846.
                                                                                                                                                                                                                                                                                                18-JUL-2001; 2001US-0306220P.
                                                                                                                                                                                                                                                                                                                       (MILL-) MILLENNIUM PHARM INC
                                                                                         ACN83021 standard; DNA; 869
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                                                                                                                                     (first entry)
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Best Local Similarity
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                                                                                                                                                                                                                               US2003099974-A1.
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                                                                                                                                                                                                                                                                                                                                           Lillie J,
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                                                                                                                ACN83021;
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                                                                                                                                                                                                                                                                                                                                                                                                                   cancer
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                                                                               ACN8302
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net positive or net negative charge during sequencing. The recombinant thermostable DNA polymerases are useful in many recombinant DNA techniques, e.g. nucleic acid amplification by polymerase chain reaction, self-sustained sequence replication, or high temperature DNA sequencing. The recombinant thermostable DNA polymerases are also useful in increasing the uniformity of dye-terminator incorporation in fluorescent depends a sequencing. The present sequence represents a sequence obtained
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polymerases having an amino acid substitution at E681. The new DNA bolymerases have improved discrimination properties (and thus resulting in improved signal uniformity) and increased tolerance to high salt conditions. They also modulate the incorporation of terminators having a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New purified recombinant thermostable DNA polymerases having amino acid substitutions at E410R or E681R, useful in recombinant DNA techniques, e.g. nucleic acid amplification or high temperature DNA sequencing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    specification describes new purified recombinant thermostable DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           after sequencing with a modified Tag DNA polymerase of the invention
                                    pREFY2pref;
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   polymerase; signal uniformity; salt tolerance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ACTIPAGGITATAGGGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
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Thermostable DNA polymerase; signal uniformity; salt tol
nucleic acid amplification; polymerase chain reaction; p
self-sustained sequence replication; DNA sequencing; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nampalli S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Finn PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AMSH ) AMERSHAM PHARMACIA BIOTECH INC.
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                                                                                                                                                                                                             WO200114568-A1
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17-SEP-1999;
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                                                                                                                                        Unidentified
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The invention relates to nucleic acid markers which are overexpressed in cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the necoded by the markers, antibodies that selectively bind to the polypeptides of developing ovarian cancer involving inhibiting expression of a gene corresponding ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and amethod of treating a patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer comparing the level of expression of a marker in a patient sample and a normal level of expression of a marker in a patient sample and an ormal level of expression of a marker in a control non-ovarian cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of a marker is assessed by detecting the presence of the marker is assessed by detecting the presence of protein or protein fragment is detected using an antibody that specifically binds with the protein or protein the assession of the marker is assessed by detecting the presence of a transcribed the protein or protein the sample is detected using an antibody that specifically binds with the protein or protein and a patient of a patient o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polynucleotide which anneals with the marker or anneals with a portion of the polynucleotide comprising the marker, under stringent conditions. The marker is also used for monitoring the progression of ovarian cancer in a patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out
                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents a human ovarian cancer DNA marker of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 13142; 106pp; English.
                                                                                                                                                                                                                               (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                15-JUN-2000; 2000US-0211940P. 07-JUL-2000; 2000US-0216820P.
                                                                                                                                25-JUL-2000; 2000US-0220661P
21-DEC-2000; 2000US-0257672P
                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-611502/70
                                                                                                                                                                                                                                                                                               Lillie J;
21-MAR-2000;
25-MAY-2000;
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                                                                                                                                                                                                                                                                                               Lee J,
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ö Gaps . 0 71.2%; Score 35.6; DB 5; Length 586; 82.0%; Pred. No. 6.7e-05; tive 0; Mismatches 9; Indels ( Sequence 586 BP; 168 A; 131 C; 141 G; 146 T; 0 U; 0 Other; 41; Conservative Local Similarity Query Match Matches

to treat ovarian cancer.

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516 ArriaArrecerrecercacrececerrrecaerceesaaacerere 565
1 ACTTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 50
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DNA encoding novel human diagnostic protein #13360. 13-FEB-2002 (first entry) AAS77556; 

AAS77556 standard; cDNA; 1637 BP

Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder; ss.

DNA encoding novel human diagnostic protein #13349.

(first entry)

13-FEB-2002

AAS77545;

AAS77545 standard; cDNA; 1695 BP

RESULT 10 AAS77545/

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Human; chromosome mapping; gene mapping; gene therapy; forensic;
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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging colypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other trails to assess biodiversity and to produce other types of data and products dependent on DNA and and anino acid sequences. Assets of the represent novel human diagnostic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed execution.
food supplement; medical imaging; diagnostic; genetic disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 13360; 103pp; English.
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                                                                                                                                                                            30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                      31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
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                                                                                      WO200175067-A2
                                              Homo sapiens.
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Homo sapiens.

11-OCT-2001

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this electronic format directly from WIPO at the printed specification, but was obtained in electronic format directly from WIPO at the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1183 AATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTGGGAAACCTGTCG 1134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 4942; 103pp; English.
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                                                                                                                                                              31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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82.0%;
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Best Local Similarity 82.0
Matches 41; Conservative
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                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; ABG04951.
WO200175067-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pupplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ. ID NO 13349; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                 30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                               Tang YT;
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23-AUG-2000; 2000US-00649167.
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Best Local Similarity 82.0
Matches 41; Conservative
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                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC
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Homo sapiens

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Homo sapiens.

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The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain recardion (PCR) primers, ollowers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cutivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in issue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of sites formatice for generate protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostic for generatic disorders or other traits to assess biodiversity responsible for generation of dentification of mutations responsible for generation of the invention. Note: The sequence data for this conding sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences. AAS64197-AAS94564 represent novel human diagnostic patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the equences.
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82.0%;
  30-MAR-2001; 2001WO-US008631.
                                               31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                                                     (HYSE-) HYSEQ INC
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food supplement; medical imaging; diagnostic; genetic disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding novel human diagnostic protein #23327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35.6; DB 5;
Pred. No. 9.6e-05;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 13351; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAS87523 standard; cDNA; 2424 BP
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82.0%;
                                             30-MAR-2001; 2001WO-US008631
                                                                                            2000US-00540217
2000US-00649167
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Best Local Similarity 82.0.
Local 41; Conservative
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P-PSDB; ABG13360.
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                                                                                                                                                                  HYSE-) HYSEQ INC.
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                                                                                               31-MAR-2000;
23-AUG-2000;
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11-OCT-2001
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Local Similarity 82.0 les 41; Conservative
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                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1080 AATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 1031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ACTTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2710 BP; 615 A; 724 C; 690 G; 681 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel DNA-related contig nucleotide sequence #455.
                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 13365; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADE09733 standard; DNA; 2710 BP
31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                   Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-DEC-2002; 2002WO-US039555.
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11-DEC-2001; 2001US-0339453P.
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                                                                                                                  2001-639362/73
                                                                                 Liu C,
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Best Local Similarity
Matches 41; Conserv
                                                  (HYSE-) HYSEQ INC
                                                                                                                                  P-PSDB; ABG13374
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                                                                                                                                                                                                                  biodiversity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-JAN-2004
                                                                                 Drmanac RT,
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ADE09733/c
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The invention comprises the amino acid and coding sequences of novel proteins. The DNA and protein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to genetic disorders. The present DNA sequence in patients to identify potential exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            analysis, characterization or therapeutic use, or as markers for tissues
in which the corresponding protein is preferentially expressed.
                                                                                                                                                                                                                                                                            Wang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotides, useful for expressing recombinant proteins for
                                                                                                                                                                                                                                                                            Zhao QA,
                                                                                                                                                                                                                                                                         Zhang J, Zhao QA,
ou P, Drmanac RT,
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                                                                                                                                                                                                                                               Ren F, Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 2277; 1177pp; English.
                                                                                                                                                                                                                                                                                                      Weng G, Zh
Boyle BJ;
                                                                                                                                                                                                                                                                            Goodrich RW,
                                                                                                                                                                                                                                                                      Tang YT, Asundi V, Goodrich R
Ghosh M, Xue AJ, Wehrman T,
Ma Y, Wang D, Chen R, Xu C,
                                                      12-APR-2002; 2002US-03723B1P.
12-ARR-2002; 2002US-0372B1SP.
22-APR-2002; 2002US-0012B55B.
24-APR-2002; 2002US-0376045P.
2002US-0365091P.
                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-569235/53.
                                                                                                                                                                                                               (HYSE-) HYSEQ INC.
                         14-MAR-2002;
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1080 AATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 1031 1 ACTTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG

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Gaps

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Indels

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71.2%; Score 35.6; DB 10 82.0%; Pred. No. 9.9e-05; ative 0; Mismatches 9

DB 10; Length 2710;

Search completed: May 10, 2005, 04:32:55 Job time : 61.6776 secs

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7, Appli 3, Appli 16, Appl 11, Appl 11, Appl 6, Appli 19, Appl 14, Appl 15, Appl 15, Appl 15, Appli 8, Appli

ALIGNMENTS

Sequence Seq

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US-09-736-447-639
US-09-611-1248-639
US-09-671-325-639
US-09-589-184-639
US-09-334-818A-7
US-09-334-818A-10
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Sequence 117, Appl
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Compugen Ltd
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US-08-133-011-114

US-08-132-730A-114

US-08-387-9575-41

US-08-387-975-41

US-08-99-575-41

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US-08-99-575-41

US-08-99-575-41

US-08-99-575-41

US-08-383-619-114

US-08-331-132-1

US-08-531-132-1

US-08-128-173A-1

US-10-165-887-2

US-10-165-887-2

US-09-525-046-3

US-09-525-046-3

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Sequence 1, Application US/08778217   Sequence 1, Application US/08778217   Sequence 1, Application US/08778217   Sequence 1, Application US/0877821   Sequence 1, Application US/0878213   TITLE OF INVERTION: Highly-Purified Recombinant TITLE OF INVERTION: Highly-Purified Recombinant TITLE OF INVERTION: ADDRESS: 0	0/1-210-025-00-311				
MANTION:  Racian et al.  Racian et al.  NUENTION: Highly-Purified Recombinant  NUENTION: Reverse Transcriptase  SEQUENCES: 13  ENCE ADDRESS:  E Gan-Probe Incorporated  10210 Genetic Center Drive  an Diego  California  10210 Genetic Center Drive  an Diego  California  1021-4362  EADABLE FORM:  EADABLE FORM:  EADABLE FORM:  SASTEM: Microsoft MS-DOS (Version 6.0)  PLICATION DATA:  ION NUMBER: US/08/778,217  ATE: January 9, 1997  ATE: January 9, 1997  ATE: January 9, 1997  ATE: April 1, 1994  ATE: April 1	Sequence 1, Applicat	ion US/08778217			
Kacian et al.  NVENTION: Highly-Purified Recombinant NVENTION: Highly-Purified Recombinant NVENTION: Highly-Purified Recombinant SEQUENCES: 13 ENCE ADDRESS: ENC ADDRESS: ENCE ADDRESS: ENCE ADDRESS: ENCE ADDRESS: ENCE ADDRESS: ENCE ADDRESS: ENC ADDRESS: E	; Patent: No. 5935833 ; GENERAL INFORMATION	••			
WYENTION: REVERSE Transcriptage SEQUENCES: 13 ENCE ADDRESS: EN Gen-Probe Incorporated 10210 Genetic Center Drive an Diego California USA 1214362 EAGABALE FORM: THE COMPAIRED TO CONTROL OF THE CONTROL OF THE CALL OF THE CAL	APPLICANT: Kacia	a .			
SEQUENCES: 13  ENCE ADDRESS:  ENCE ENC ENCE ADDRESS:  ENCE ADDRESS:  ENCE ADDRESS:  ENCE ADDRESS:  ENC ENC ADDRESS:  ENC E	; TITLE OF INVENTIO				
E: Gen-Probe Incorporated 10210 Genetic Center Drive 10210 Genetic Center Drive 10210 Genetic Center Drive 10213 USA 1028A 1038A 103	, NUMBER OF SEQUENC	ES: 13 DRESS:			
10210 Genetic Center Drive an Diego California USA 12.14362 EADABLE PORM: YPE: 3.5" Diskette, 1.44 Mb storage : IBM compatible G SYSTEM: SATSEQ PLICATION DATA: ICATION NUMBER: 08/221,804 AGE: April 1, 1994 GENT INFORMATION: ICATION NUMBER: 40,627 ELOCKET NUMBER: MOL2A-A01F01 ICATION NUMBER: MOL2A-A01F01 ICATION NUMBER: MOL2A-A01F01 ICATION NUMBER: MOL2A-A01F01 ICATION NUMBER: MOLSA-B01F01 ICATION NUMBER: MOLSA-B01F01 ICATION NUMBER: MOLSA-B01F01 ICATION NUMBER: MOLSA-B01F01 ICATION NO: 92828 FOR SEQ IDNO: 1: HARACTERISTICS: 114 NESS: single : linear Innear  70.4%; Score 35.2; DB 2; Length 114; milarity 83.3%; Pred. NO: 9.6-06; CONSERVATION 0: Mismatches 8; Indels 0;	, ADDRESSEE: Gen	-Probe Incorporated			
an Diego California USA 121-4362 EADABLE PORM: EADABLE PORM: EADABLE PORM: I IBM compatible G SYSTEM: Microsoft MS-DOS (Version 6.0) FASTENG ION NUMBER: US/08/778,217 CATION: ICATION DATA: ICATION DATA: including application ICATION DATA: described below: ICATION DATA: described below: ICATION DATA: MOL21,804 ATE: April 1, 1994 ATE: April 1, 1994 ATE: MOL2A-A01F01 ICATION NUMBER: WOL2A-A01F01 ICATION INFORMATION: E: (619) 410-8926 FOR SEQ ID NO: 1: HARACTERISTICS: ILINEAR ILINEAR  NO: 48; SCOIR 35.2; DB 2; Length 114; milarity 83.3%; Pred: No: 9.6e-06; CONSERVATIVE 0; Mismatches 8; Indels 0;	; STREET: 10210	Genetic Center Drive			
California 121-4362 EADABLE FORM: EADABLE FORM: 1 IBM compatible G SYSTEM: Microsoft MS-DOS (Version 6.0) ELICATION DATA: 1 ION NUMBER: US/08/778,217 ATE: January 9, 1997 ATE: April 1, 1994 ATE: April	O)				
121-4362 EADABLE FORM: TYPE: 3. Diskette, 1.44 Mb storage G SYSTEM: Microsoft MS-DOS (Version 6.0) E-STSTEQ THE MICROSOFT MS-DOS (Version 6.0) TOWNUMBER: US/08/778,217 ATE: January 9, 1997 ATE: April 1, 1994 ATE: April 1, 1	÷				
EADABLE FORM: The compatible of SYSTEM: Microsoft MS-DOS (Version 6.0) ESASTSEQ G SYSTEM: Microsoft MS-DOS (Version 6.0) F FASTSEQ IDN NUMBER: US/08/778,217 ATE: January 9, 1997 ATE: January 9, 1994 ATE: April 1, 1994 ATE: Ap	; ZIP: 92121-436	2			
YPE: 3.5" Directre, 1.44 Mb Biorage TYPE: 1BM Compatible G SYSTEM: Microsoft MS-DOS (Version 6.0) : FRASTERO PLICATION DATA: ION NUMBER: US/08/778,217 ATE: January 9, 1997 ATE: April 1, 1994 ATE: April 1, 1	; COMPUTER READABLE	:			
G SYSTEM:  I PASTERS  E PASTERS  E PASTERS  IDIO NUMBER: US/08/778,217  ATE: January 9, 1997  CATION:  CATION DATA:  ICATION DATA:  ICATION:  ICATION:  ICATION:  ICATION NUMBER: MOL2A-A01F01  ICATION NUMBER: MOL2A-A01F01  ICATION NO. 928  ICATION OF SEQ.  ICATION ICATION:  ICATION OF SEQ.  ICATION IN CONCETTOR  ICATION OF SEQ.  ICATION OF	, MEDIUM TYPE: 3				
FASTSEQ PLICATION DATA: TOWN WIGHER: 05/08/778,217 ATE: January 9, 1997 CATION: ICATION DATA: including application ICATION DATA: including application ICATION DATA: described below: ION NUMBER: 08/221,804 ATE: April 1, 1994 GENT INFORMATION: hristine A. Gritzmacher ICATION UNMBER: MO.627 ALOCKET WINDER: MO.627 ICATION INFORMATION: E: (619) 410-8926 ICATION INFORMATI	OPERATING SYSTE	Microsoft MS-DOS (Version	â		
PLICATION DATA:  ION NUMBER: US/08/778,217  CATICN: January 9, 1997  CATICN: January 1, 1994  GENT INFORMATION: January 1, 1994  GENT INFORMATION: January 1, 1994  GENT INFORMATION: January 1, 1996  E. (G19) 410-8926  E. (G19) 410-8938  FOR SEQ ID NO: 1: January  CATICN: January  ANARCTERISTICS: January  ANARCTERISTICS: January  CATICN: January  ANARCTERISTICS: January  ANARCTERISTICS: January  ANARCTERISTICS: January  CATICN: January  ANARCTERISTICS: January  ANARCTERIS	; SOFTWARE: FAST				
ION NUMBER: US/08/778,217 CATE: January 9, 1997 CATION: ICATION DATA: including application ICATION DATA: described below: ICATION DATA: described below: ION NUMBER: 08/221,804 ATE: April 1, 1994 ATE: April 1, 1994 ATE: April 1, 1994 ATE: MOLZA-A01F01 ICATION NUMBER: WOLZA-A01F01 ICATION INFORMATION: E: (619) 410-8926 (619) 410-8926 FOR SEQ ID NO: 1: HARACTERISTICS: 1110-87 AND	; CURRENT APPLICATI	ON DATA:			
ALE: January 9, 1397  ACATION: ICATION DATA: ICATION NUMBER: 08/221,804  ATE: April 1, 1994  ATE: Ap	, APPLICATION NUM	BER: US/08/778,217			
ICATION DATA: ICATION NUMBER: ADTIL 1, 1994 GENT INFORMATION: ATE: ADTIL 1, 1994 GENT INFORMATION: ICATION NUMBER: AO.2A - AO.1FO1 E. (619) 410-8926 F.	. NOTESTATED ON THE CONTROL OF THE C	anuary 9,			
ICATION DATA: including application ICATION DATA: described below: ICATION DATA: 08/221,804  ATE: April 1, 1994 GENT INFORMATION: ACRIT. A. GFILAMACHATION: ACRIT. NUMBER: 40,627 ELOCKET NUMBER: MOLZA-A01F01 ELCATION NUMBER: MOLZA-A01F01 ELCATION INFORMATION: E: (619) 410-8928 FOR SEQ 110 NO: 1: HARACTERISTICS: 114 NESS: single : linear  10.4%; Score 35.2; DB 2; Length 114; milarity 83.3%; Pred. NO: 9.6-06; CONSERVATIVE 0; Mismatches 8; Indels 0;	PRIOR APPLICATION				
ICATION DATA: described below:  ION WUMBER: 08/221,804  ATE: April 1, 1994  GENT INFORMATION: hitschine A. Gritzmacher hitschine A. Gritzmacher TION WUMBER: 40,627  E/DOCKET WUMBER: MOL2A-A01F01  ICATION INFORMATION: E: (619) 410-8926  (619) 410-8926  FOR SEQ ID NO: 1: HARACTERISTICS: 114  ucleic acid NESS: single : linear  10.4%; Score 35.2; DB 2; Length 114; milarity 83.3%; Pred. No. 9.6e-06; CONSERVATIVE 0; Mismatches 8; Indels 0;	, PRIOR APPLICATION	including			
ION NUMBER: 02/221,804  GENT INFORMATION: hitschine A. Gritzmacher TION NUMBER: 40,627  TION NUMBER: MOLZA-A01F01  ICATION INFORMATION: E: (619) 410-8926 (619) 410-8926 FOR SEQ ID NO: 1: HARACTERISTICS: 114 ucleic acid NESS: single : linear  TO:4%; Score 35.2; DB 2; Length 114; milarity 83.3%; Pred. No. 9.6e-06; CONSERVATIVE 0; Mismatches 8; Indels 0;	, PRIOR APPLICATION	described			
ATE: April 1, 1994  ATE: April 1, 1994  hristine A. Gritzmacher  TION NUMBER: 40,627  E. CELOCKET NUMBER: MOL2A-A01F01  ICATION INFORMATION:  E. (619) 410-8926  (619) 410-8926  FOR SEQ ID NO: 1:  HARACTERISTICS: 1  114  NESS: single : linear  70.4%; Score 35.2; DB 2; Length 114;  milarity 83.3%; Pred. No. 9.6e-06;  Conservative 0; Mismatches 8; Indels 0;	, APPLICATION NUM	•			
hrietine A. Gritzmacher TION NUMBER: 40,627 E/DOCKET NUMBER: MOL2A-A01F01 E/DOCKET NUMBER: MOL2A-A01F01 E: (619) 410-8928 FOR SEQ 1D NO: 1: HARACTERISTICS: 114 NESS: single : linear 10.4%; Score 35.2; DB 2; Length 114; milarity 83.3%; Pred. No. 9.6e-06; COnservative 0; Mismatches 8; Indels 0;	FILING DATE: A	pril 1, 1994			
TION NUMBER: 40,627 E/DOCKET NUMBER: MOL2A-A01F01 ELGATION INFORMATION: E: (619) 410-8928 F(619) 410-8928 F(61	NAME: Christin	e A. Gritzmacher			
E/DOCKET NUMBER: MOLZA-A01F01 ICATION INFORMATION: E: (619) 410-8926 (619) 410-8928 FOR SEQ ID NO: 1: HARACTERISTICS: 114 ucleic acid NESS: single : linear  70.4%; Score 35.2; DB 2; Length 114; milarity 83.3%; Pred. No. 9.6e-06; Conservative 0; Mismatches 8; Indels 0;	; REGISTRATION NU	MBER: 40,627			
ICATION INFORMATION:  E: (619) 410-8926 (619) 410-828 FOR SEQ ID NO: 1: HARACTERISTICS: 11.4 ucleic acid NESS: single : linear : linear  70.4%; Score 35.2; DB 2; Length 114; milarity 83.3%; Pred. No. 9.6e-06; Conservative 0; Mismatches 8; Indels 0;	; REFERENCE/DOCKE	T NUMBER: MOL2A-A01F01			
E: (619) 410-8926 (619) 410-8926 FOR SEQ ID NO: 1: HARACTERISTICS: 114 Uclaic acid NESS: single : linear 10.4%; Score 35.2; DB 2; Length 114; milarity 83.3%; Pred. No. 9.6e-06; Conservative 0; Mismatches 8; Indels 0;	; TELECOMMUNICATION	INFORMATION:			
FOR SEQ IN 0: 1: HARACTERISTICS: 114 NESS: single 1 linear 70.4%; Score 35.2; DB 2; Length 114; milarity 83.3%; Pred. No. 9.6e-06; Conservative 0; Mismatches 8; Indels 0;	: :	7) 4TO-8V26			
HARACTERISTICS:  114  102	TNFORMATION FOR SEC	TD NO:			
ucleic acid NESS: single : linear  70.4%; Score 35.2; DB 2; Length 114; milarity 83.3%; Pred. No. 9.6e-06; Conservative 0; Mismatches 8; Indels 0;	SEOUENCE CHARACTE	ISTICS:			
ucleic acid NESS: single : linear  70.4%; Score 35.2; DB 2; Length 114; milarity 83.3%; Pred. No. 9.6e-06; Conservative 0; Mismatches 8; Indels 0;	; LENGTH: 114				
NESS: single : linear 70.4%; Score 35.2; DB 2; Length 114; milarity 83.3%; Pred. No. 9.6e-06; Conservative 0; Mismatches 8; Indels 0;	. ; TYPE: nucleic	acid			
<pre>: 11near  70.4%; Score 35.2; DB 2; Length 114; milarity 83.3%; Pred. No. 9.6e-06; Conservative 0; Mismatches 8; Indels 0;</pre>	ESS:	single			
70.4%; Score 35.2; DB 2; Length 114; Similarity 83.3%; Pred. No. 9.6e-06; Onservative 0; Mismatches 8; Indels 0;		ar.			
Similarity 83.3%; Pred. No. 9.6e-06; Onservative 0; Mismatches 8; Indels 0;	Match Watch	Score 15 2. DB 2.	.ength 114.		
40; Conservative 0; Mismatches 8; Indels 0;	Best Local Similarit	83.3%; Pred. No. 9.6e-06;			
	40;	vative 0; Mismatches	0	Gaps	

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RESULT 5
US-08-276-852-41/c
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Batent NO. 6593120

Batent NO. 6593120

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SORENSEN, Matthew
TITLE OF INVENTION: RECOMBINANT DNA ENCODING REVERSE TRANSCRIPTASE DERIVED FROM TITLE OF INVENTION: MOLONEY MURINE LEUKEMIA VIRUS
FILE REFERENCE: GP059-05-CP1
CURRENT APPLICATION NUMBER: US/09/397,955C
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 08/821,948
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APPLICATION NUMBER: US/08/821,948
FILING DATE:

APLICATION NUMBER: US/08/821,948
FILING APPLICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/43,781
FILING DATE: May 18, 1994

ATTORNEY, AGENT INFORMATION:

REGISTATION NUMBER: 40,627

REFERENCE/DOCKET NUMBER: MOLZA (New Ref.: GP059-04.FW2)

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70.4%; Score 35.2; DB 2; Length 114; 83.3%; Pred. No. 9.6e-06;
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63 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 16
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: 18M compatible
OPERATING SYSTEM: Microsoft MS-DOS (Version 6.0)
                                                                                                                                                                                                                                                                         Sequence 1, Application US/08821948.

Patent No. 5998195.

GENERAL INFORMATION:
APPLICANT: Racian et al.
TITLE OF INVENTION: Highly-Purified Recombinant
TITLE OF INVENTION: Reverse Transcriptase
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Gen-Probe Incorporated
STREET: 10210 Genetic Center Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 70.4
Best Local Similarity 83.3
Matches 40; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: San Diego
STATE: California
COUNTRY: USA
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Gaps
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COTHER INFORMATION: Oligonucleotide used to construct plasmid pUC 18N
US-09-397-955C-1
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Patent No. 5652138

GENERAL INFORMATION:
APPLICANT: Burron, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNOBFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
70.4%; Score 35.2; DB 4; Length 114;
Best Local Similarity 83.3%; Pred. No. 9.6e-06;
Matches 40; Conservative 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: HIGHLY-PURIFIED RECOMBINANT REVERSE TITLE OF INVENTION: TRANSCRIPTASE NUMBER OF SEQUENCES: 18 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 SOFTWARE:
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APPLICATION NUMBER: PCT/US95/04092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT-US95-04092-1/c
; Sequence 1, Application PC/TUS9504092
; GENERAL INFORMATION:
; APPLICANT:
PRIOR APPLICATION NUMBER: 08/443,781
PRIOR FILING DATE: 1995-05-18
PRIOR APPLICATION NUMBER: 08/221,804
PRIOR FILING DATE: 1994-04-01
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 1
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Best Local Similarity 83.3%;
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
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CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 118 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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65 rhaarrecerrecercachecececrrrecaerceeaaacerere 18
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Patent No. 5759817
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: HETERODIMERIC RECEPTOR LIBRARIES USING
TITLE OF INVENTION: PHAGEMIDS
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scrippe Research Institute, Office of
ADDRESSEE: Patent Counsel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5759817th Torrey Pines Road, Suite 220,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/322,730A
SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35.2; DB 1;
Pred. No. 1.1e-05;
0; Mismatches 8;
                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 10-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/683,602
FILING DATE: 27-JAN-1992
PRIOR APPLICATION NUMBER: PCT/US 92/03091
APPLICATION NUMBER: PCT/US 92/03091
ATTORNE: FILLING DATE: 10-APR-1992
ATTORNE: FILLING, Thomas
NAME: FILLING, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/826,623
FILING DATE: 27-7AN-1992
APPLICATION NUMBER: US 07/683,602
FILING DATE: 10-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                SCRF 238.2
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10-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEG ID NO: 114: SEQUENCE CHARACTERISTICS: LENGTH: 201 base pairs TYPE: nucleic acid sTRANDEDNESS: double TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-6312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 70.4%;
Best Local Similarity 83.3%;
Matches 40; Conservative
                                                                08-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 10550 No. 5759
STREET: Mail Drop TPC8
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: La Jolla
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 7
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| Patent No. 5658727
| GENERAL INPORMATION:
| APPLICANT: Rang, Angray
| APPLICANT: Barbas, Carlos
| APPLICANT: Lerner, Richard A.
| TILLE OF INVENTION: HETERODIMERIC RECEPTOR LIBRARIES USING: TITLE OF INVENTION: PHAGEMIDS
| NUMBER OF SEQUENCES: 161
| CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: ADDRESSE: Phe Scripps Research Institute, Office of ADDRESSE: Patent Counsel
| STREET: 1066 No. 5658727th Torrey Pines Road, TPC-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel STREET: 10666 No. 5652138th Torrey Pines Road, Suite 220, STREET: Mail Drop TPC8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Indels
                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 18-JUL-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 35.2; DB 1;
Pred. No. 1.1e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-5EP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-5EP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTATION NUMBER: 34,1633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: SC
TELECOMMUNICATION INFORMATION
TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 70.4%;
Best Local Similarity 83.3%;
Matches 40; Conservative
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TELBERA: 619-554-6312
INFORMATION FOR SEQ ID NO: 41
SEQUENCE CHARACTERISTICS:
LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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MOLECULE TYPE: DN
                                                                                       La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: N
ANTI-SENSE: NO
US-08-276-852-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-133-011-114/c
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Gaps

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Indels

Length 201;

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TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
  DNA (genomic)
NO
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                                                                                                           70.4%;
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SEQUENCE CHARACTERISTICS:
LENGTH: 201 base pairs
                                                                                                                                                         40; Conservative
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STRANDEDNESS: double
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                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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STATE: CA
  MOLECULE TYPE:
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                                           ; ANTI-SENSE:
US-08-387-874-87
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                                                                                                                                                         Matches
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Patent No. 5770356

GENERAL INFORMATION:
APPLICANT: Light, Paul L., II
APPLICANT: Light, Paul L., II
APPLICANT: Lerner, Richard A.
TITLE OF INVENTION: RECEPTOR AND A SURFACE HETEROLOGOUS PROTEIN
NUMBER OF SEQUENCES: 97
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5770356th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,874
FILING DATE: 22-FEB-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US93/08364
FILING DATE: 03-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,369
FILING DATE: 04-SEP-1993
PILING DATE: 04-SEP-1992
ATFORMEY/AGENT INPORMATION:
ANAME: G16-Live Thromas
                                                                SCR0707P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TERI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-6312
                  NAME: Bingham, Douglas A
REGISTRATION NUMBER: 32,457
REFERENCE/DOCKET NUMBER: SCRO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-784-9397
TELEPAX: 619-784-9399
                                                                                                                                                     INFORMATION FOR SEQ ID NO: 114: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                              LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                   õ
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HYPOTHETICAL:
HYPOTHETICAL:
NO-08-322-730A-114
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                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Burton, Dennis R
APPLICANT: Burton, Dennis R
APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Barbas, Carlos F
APPLICANT: Bribard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNOBERCIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 NO. 5770440th Torrey Pines Road, Suite 220,
STREET: Mail Drop IPC8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 70.4%; Score 35.2; DB 1; Length 201; Best Local Similarity 83.3%; Pred. No. 1.1e-05; Matches 40; Conservative 0; Mismatches 8; Indels (
   Length 201;
                                                                                                                        3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 50
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                                                               Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION NUMBER: US 08/276,852
PRIOR APPLICATION NUMBER: US 08/276,852
PRIOR APPLICATION NUMBER: US 08/178,302
RILNG DATE: 30-SEP-1993
PRIOR APPLICATION NUMBER: US 08/178,302
RILNG DATE: 30-SEP-1993
PRIOR APPLICATION NUMBER: US 07/954,148
RILNG DATE: 30-SEP-1993
APPLICATION NUMBER: US 07/954,148
RILNG DATE: 30-SEP-1992
Score 35.2; DB 1;
Pred. No. 1.1e-05;
0; Mismatches 8;
                                                                                                                                                                                                                                                                                                               Sequence 41, Application US/08899575
Patent No. 5770440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCI
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92037
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                                                                                                                                                                                                                                                                                                                                              HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
                                                                                                                                                                                                                                                    APPLICANT: Burbas, Carlos F
APPLICANT: Barbas, Carlos F
APPLICANT: Barbas, Carlos F
APPLICANT: Berner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIE:
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESSS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 70.4%; Score 35.2; DB 1; Length 201; Best Local Similarity 83.3%; Pred. No. 1.1e-05; Matches 40; Conservative 0; Mismatches 8; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65 riparrecerrécercacrececerriceacrecesanes 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TEM PC compatible
CORPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1993
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INPORMATION:
NAME: APPLICATION THOMSE
                                                 65 rraarrecerrecerrecrecrececrrrecaercegaaace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TTAAGCTTATAGCGATGACTGCCCGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-383-619-114/c
; Sequence 114, Application US/08383619
; Patent No. 5955341
                                                                                                                                                                               Sequence 41, Application US/08899575
Patent No. 5804440
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 41: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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HYPOTHETICAL: 1
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APPLICANT: Barbas, Carlos
APPLICANT: Barbas, Carlos
APPLICANT: Lerner, Richard
TITLE OF INVENTION: HETERODIMERIC RECEPTOR LIBRARIES USING
TITLE OF INVENTION: PHAGEMIDS
NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
CORRESPONDENCE DOUGLAS A. BINGHAM
STREET: 11300 Sorrento Valley Road, Suite 200
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92121
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/383,619
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APPLICANT: Barbas, Carlos
APPLICANT: Barbas, Carlos
APPLICANT: Barbas, Carlos
APPLICANT: Barbas, Carlos
APPLICANT: Lerner, Richard A.
TITLE OF INVENTION: PHACEMIDS
NUMBER OF SEQUENCES: 161
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel
STREET: 10666 No. 6235469th Torrey Pines Road, TPC-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: US/08/126,680
FILING DATE:
APPLICATION NUMBER: US/07/683,602
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bingham, Douglas A.
REGERENCE/DOCKET NUMBER: SCR0371P
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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; Sequence 114, Application US/08907739
; Patent No. 6235469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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US-08-383-619-114
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TITLE OF INVENTION: PHAGEMIDS COEXPRESSING A SURFACE
TITLE OF INVENTION: RECEPTOR AND A SURFACE HETEROLOGOUS PROTEIN
NUMBER OF SEQUENCES: 97
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08364
FILING DATE: 03-SEP-1993
PRIOR APPLICATION NUMBER: US7/91/941,369
FILING DATE: 04-SEP-1992
INFORMATION FOR SEQ ID NO: 87:
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70.4%; Score 35.2; DB 5;
Best Local Similarity 83.3%; Pred. No. 1.1e-05;
Matches 40; Conservative 0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 35.2; DB 3;
Pred. No. 1.1e-05;
0; Mismatches 8;
                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET WUMBER: SCRF 238.2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
                                             FILING DATE: 1994-09-29
APPLICATION NUMBER: US 07/826,623
FILING DATE: 27-JAN-1992
FILING DATE: 10-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 114:
                          08/133,011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 87, Application PC/TUS9308364 GENERAL INFORMATION: APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                   TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA (genomic)
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Best Local Similarity 83.3%;
Matches 40; Conservative
    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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PCT-US93-08364-87/c
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PCT-US93-08364-87
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Barbas, Carlos
Lerner, Richard A.
TITLE OF INVENTION: HFTERODIMERIC RECEPTOR LIBRARIES USING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 161
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 10666 No. 6468738th Torrey Pines Road, TPC-8 STREE CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 70.4%; Score 35.2; DB 3; Length 201; 1 Similarity 83.3%; Pred. No. 1.1e-05; 40; Conservative 0; Mismatches 8; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/907,739
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APPLICATION NUMBER: US/09/729,597
FILING DATE: 04-Dec-2000
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/826,623
FILING DATE: 27-JAN-1992
PRIOR APPLICATION DATE:
PAPPLICATION NUMBER: PCT/US 92/03091
FILING DATE: 10-APR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 114, Application US/09729597 Parent No. 6468738 GENERAL INFORMATION:
                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/133,011
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFRENCE/DOCKET NUMBER: SCRF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 92037
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 201 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                             COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 40; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                      CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE: NO
US-08-907-739-114
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US-09-729-597-114/c
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RESULT 15
PCT-US95-08743-41/C

FCT-US95-08743-41/C

SEQUENCE 41, Application PC/TUS9508743

GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNDEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 11-JUL-1995
FILING DATE: 16-JUL-1994
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERIFETICS:
LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
TYPE: NO GENORIC TYPE: DNA (Genomic)
HYPOTHETICAL: NO
ANTI-CENSER. NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
70.4%; Score 35.2; DB 5; Length 201;
Best Local Similarity 83.3%; Pred. No. 1.1e-05;
Matches 40; Conservative 0; Mismatches 8; Indels C
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Gaps

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Search completed: May 10, 2005, 07:29:36 Job time : 17.6245 secs

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May 10, 2005, 05:52:55 ; Search time 141.277 Seconds (without alignments) 2164.037 Million cell updates/sec
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cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
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cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
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cgn2_6/ptodata/1/pubpna/US10_RWPUB.seq:*
cgn2_6/ptodata/1/pubpna/US10_RWPUB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCT NEW PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/USO8_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*

8: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

8: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
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ptodata/1/pubpna/US10B PUBCOMB.seq:*
ptodata/1/pubpna/US10C PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /pubpna/US09B_PUBCOMB.seq:*/pubpna/US09C_PUBCOMB.seq:*/pubpna/US09_NEW_PUB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUBCOMB.seq:*
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## SUMMARIES

	Description	Semience 10 Appl	Sequence 37. Appl	Sequence 7241, Ap	Sequence 4171, Ap	Sequence 80752, A	Sequence 13142, A	Sequence 2086, Ap	Sequence 2087, Ap	Sequence 2086, Ap	Sequence 2087, Ap	Sequence 88806, A
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Gaps
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                                                                                                                                                                                                                                                          , NAME/KEY: misc_feature
; LOCATION: 282, 300, 554, 592, 650, 707, 720, 728, 755, 767, 775, 791
; CTHER INFORMATION: n = A.T.C or G
US-10-199-846-7241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , COMPOSITIONS, KITS, AND METHODS FICATION, ASSESSMENT, PREVENTION, AND
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                                                                                                                                                                                                                                                                                                                                                                                    Query Match 71.6%; Score 35.8; DB 14; Length 791; Best Local Similarity 83.3%; Pred. No. 4e-05; Matches 40; Conservative 0; Mismatches 8; Indels 0.
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APPLICANT: Millie, James
APPLICANT: Wangy o
APPLICANT: Wangy o
APPLICANT: Wangy o
APPLICANT: Wangy o
APPLICANT: Wangy Youzhen
APPLICANT: Wangy Youzhen
APPLICANT: Yeinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, K:
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MKI-049
CURRENT APPLICATION NUMBER: US/10/198, 846
CURRENT APPLICATION NUMBER: 0002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILLING DATE: 2001-07-18
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 7241
LENGTH: 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4171
LENCTH: 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) NAME/KEY: misc_feature
; LOCATION: 2, 3, 4, 6, 9, 10, 11, 531, 5;
; LOCATION: 763, 764, 780, 816, 841, 856
; OTHER INFORMATION: n = A,T,C or G
US-10-198-946-4171
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; Sequence 80752, Application US/10437963
; Publication No. US20040123343A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4171, Application US/10198846 Publication No. US20030099974A1 GENERAL INFORMATION:
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Best Local Similarity 83.3'
Matches 40; Conservative
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                                                                                                                                                                                   TYPE: DNA ORGANISM: Homo sapiens
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APPLICANT: Wang, Youzhen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MII-049
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                                                                                 APPLICANT: Rosen et al.
TITLE OF INVENTION: 33 Human Secreted Proteins
FILE REFERENCE: PZ036P1
                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/985,153
CURRENT FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: 09/618,150
PRIOR FILING DATE: 2000-07-17
PRIOR PELICATION NUMBER: PCT/US00/00903
PRIOR FILING DATE: 2000-01-18
PRIOR FILING DATE: 1999-01-19
PRIOR PLILING DATE: 1999-01-19
NUMBER OF SEQ ID NOS: 147
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 37
LENGTH: 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: n equals a,t,g, or c
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OTHER INFORMATION: n equals a,t,g, or
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Publication No. US20030099974A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (113)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: SITE
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Sequence 37, Application US/09985153 Publication No. US20040181047A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (27)
OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (163)
OTHER INFORMATION:
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (727)
OTHER INFORMATION:
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APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K. APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua APPLICANT: Cao, Yongwei

GENERAL INFORMATION:

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GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-24
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-11-23
PRIOR PLING DATE: 1999-11-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 71.2%; Score 35.6; DB 13; Best Local Similarity 82.0%; Pred. No. 5e-05; Matches 41; Conservative 0; Mismatches 9;
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Publication No. US20020198371A1
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i LOCATION: (1)...(865)

i OTHER INFORMATION: n = A,T,C or G

US-10-027-622-2086
       US20020198371A1
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ORGANISM: Human
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                                                                                                APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 80752
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; Publication No. US20030165831A1
; Gequence 13142, Application US/09814353
; Publication No. US20030165831A1
; GERRAAL INFORMATION:
   APPLICANT: Liblie, James
   APPLICANT: Liblie, Jam
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.2%; Score 35.6; DB 18; Length 415; 82.0%; Pred. No. 4.4e-05; tive 0; Mismatches 9; Indels 0
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Pred. No. 4.6e-05;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_80346C.1
US-10-437-963-80752
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SOFTWARE: FastSEQ for Windows Version 4.0
Wu, Wei
Boukharov, Andrey A.
Barbazuk, Brad
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71.2%;
Best Local Similarity 82.0%;
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 82.09
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Oryza sativa
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US-09-814-353-13142
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US-10-027-632-2086/c
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RESULT 12
US-10-437-963-39259/c
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: DOLYMORPHISMS in the Human Genome
FILE REFERENCE: 10827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT PILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/128,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-24
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/166,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR PILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FASELSEQ FOR Windows Version 4.0
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108627.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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71.2%; Score 35.6; DB 17; Length 865;
Best Local Similarity 82.0%; Pred. No. 5e-05;
Matches 41; Conservative 0; Mismatches 9; Indels 0;
                                                                                                                                                                              5; DB 13; Length 865;
5e-05;
thes 9; Indels 0
                                                                                                                                                                              ; Score 35.6; DB;
; Pred. No. 5e-05
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2086, Application US/10027632 Publication No. US20030204075A9 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . ...... (1)...(865)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-2086
                                                                          LOCATION: (1) ... (865)

OTHER INFORMATION: n = A,T,C or G
US-10-027-632-2087
                                                                                                                                                                                 Query Match
Best Local Similarity 82.0%;
Matches 41; Conservative
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                                                    NAME/KEY: misc feature
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US-10-027-632-2087/c
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ORGANISM: Human
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APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Buckharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 88806
LENGTH: 2307
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71.2%; Score 35.6; DB 17; Length 865;
Best Local Similarity 82.0%; Pred. No. 5e-05;
Matches 41; Conservative 0; Mismatches 9; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ACTTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
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6e-05;
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1 Similarity 82.0%; Pred. No. 6e-0
41; Conservative 0; Mismatches
                  PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-12-3
PRIOR FILING DATE: 1999-18
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-3
NUMBER OF SEQ ID NOS: 325720
SEQ ID NO 2087
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APPLICATION NUMBER: US 60/218,006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 88806, Application US/10437963 Publication No. US20040123343A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  i LOCATION: (1)...(865)
i OTHER INFORMATION: n = A,T,C or G
US-10-027-632-2087
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
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Matches 41, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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APPLICANT: Schleget. Kousert
APPLICANT: Schleget. Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REFERENCE: MXI-007BCN
CURRENT PAPLICATION NUMBER: 09/785,276
FRIOR FILING DATE: 2003-02-04
FRIOR PELING DATE: 2000-02-17
FRIOR PELING DATE: 2000-02-17
FRIOR PELING DATE: 2000-02-17
FRIOR PELING DATE: 2000-03-16
FRIOR PELING DATE: 2000-05-25
FRIOR PELING DATE: 2000-06-25
FRIOR PELING DATE: 2000-06-28
FRIOR PELING DATE: 2000-06-29
FRIOR PELING DATE: 2000-06-25
FRIOR PELING DATE: 2000-06-29
FRIOR PELING DATE: 2000-07-30
FRIOR PELING DATE: 2000-
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Fatent No. US20020102638A1

GENERAL INFORMATION:

APPLICATION: Rosen et al.

TITLE OF INVENTION: NUMBER: US/09/764,846

CURRENT APPLICATION NUMBER: US/09/764,846

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper; NUMBER OF SEQ ID NOS: 348

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 347

LENGTH: 195
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                                                  3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
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NAME/KEY: SITE
LOCATION: (159)
OTHER INFORMATION: n equals a,t,g, or NAME/KEY: SITE
                                                                                                                                                                                                                                                                            Sequence 45266, Application US/10357930
Publication No. US20040259086A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Schlegel. Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 40; Conserv
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US-10-357-930-45266
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US-09-764-846-347
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 39259
LENGTH: 2721
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APPLICANT: SCRIEGE, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMAN PROSTATE CANCER
FILE REPERENCE: MRI-00790CM
CURRENT APPLICATION NUMBER: 09/185,276
PRIOR FILING DATE: 2003-02-04
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: 60/189,862
PRIOR PELING DATE: 2000-03-16
PRIOR FILING DATE: 2000-03-16
PRIOR PELING DATE: 2000-06-02-17
PRIOR APPLICATION NUMBER: 60/219,307
PRIOR PELING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-06-09
PRIOR FILING DATE: 2000-01-13
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-31
PRIOR FILING DATE: 2000-01-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ACTTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , OTHER INFORMATION: Clone ID: PAT_MRT4530_42817C.1
US-10-437-963-39259
Sequence 39259, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 36271, Application US/10357930 Publication No. US20040259086A1 GENERAL INFORMATION: APPLICANT: Schlegel. Robert
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Best Local Similarity 83.3
Matches 40; Conservative
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Gaps
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CTHER INFORMATION: n equals a,t,g, or c
NAME/KEX: SITE
LOCATION: (166)
COTHER INFORMATION: n equals a,t,g, or c
LOCATION: (193)
COTHER INFORMATION: n equals a,t,g, or c
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Search completed: May 10, 2005, 10:29:04 Job time: 142.277 secs

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1: \(\cggn2 \) \( \) \(\text{Ft} \) \(\text{ComB} \) \(\text{Seq} : * \) \(\cggn2 \) \( \) \(\text{Ft} \) \(\text{ComB} : \text{Seq} : * \) \(\cggn2 - 6 \) \(\text{Ft} \) \(\text{Pt} \) \(\text{ComB} : \text{Seq} : * \) \(\cggn2 - 6 \) \(\text{Pt} \) \(\text{ComB} : \text{Seq} : * \) \(\cggn2 - 6 \) \(\text{Pt} \) \(\text{ComB} : \text{Seq} : * \) \(\cggn2 - 6 \) \(\text{Pt} \) \(\text{ComB} : \text{Seq} : * \) \(\cggn2 - 6 \) \(\text{Pt} \) \(\text{Codata} = 1 \) \(\text{Pma} \) \(\text{USOB} \) \(\text{COMB} : \text{Seq} : * \) \(\cggn2 - 6 \) \(\text{Pt} \) \(\text{Codata} = 1 \) \(\text{Pma} \) \(\text{USOB} \) \(\text{COMB} : \text{Seq} : * \) \(\text{Seq} : * \) \(\text{Com2} - 6 \) \(\text{Pt} \) \(\text{Codata} = 1 \) \(\text{Pma} \) \(\text{USOB} \) \(\text{COMB} : \text{Seq} : * \) \(\text{Seq} : * \) \(\text{Com2} - 6 \) \(\text{Pt} \) \(\text{Codata} = 1 \) \(\text{Pma} \) \(\text{USOB} \) \(\text{COMB} : \text{Seq} : * \) \(\text{Seq} : * \) \(\text{Com2} - 6 \) \(\text{Pt} \) \(\text{Codata} = 1 \) \(\text{Pma} \) \(\text{USOB} \) \(\text{COMB} : \text{Seq} : * \) \(\text{Seq} : * \) \(\text{Com2} - 6 \) \(\text{Pt} \) \(\text{Codata} = 1 \) \(\text{Pma} \) \(\text{USOB} \) \(\text{COMB} : \text{Seq} : * \) \(\text{Seq} : * \) \(\text{Com2} - 6 \) \(\text{Pt} \) \(\text{Codata} = 1 \) \(\text{Pma} \) \(\text{USOB} \) \(\text{COMB} : \text{Seq} : * \) \(\text{Seq} : * \) \(\text{Com2} - 6 \) \(\text{Pt} \) \(\text{Codata} = 1 \) \(\text{Pma} \) \(\text{USOB} \) \(\text{COMB} : \text{Seq} : * \) \(\text{Seq} : * \) \(\text{Com2} - 6 \) \(\text{Pt} \) \(\text{Codata} = 1 \) \(\text{Pma} \) \(\text{USOB} \) \(\text{COMB} : \text{Seq} : * \) \(\text{Seq} : * \) 
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ptodata/1/pna/US096D_COMB.seq:
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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pna/US105A_COMB.seq:*
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pna/US6025_COMB.seq:
pna/US6026_COMB.seq:
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117: /cgn2_6/ptodata/1/pna/US6047_COMB.seq:*
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129: /cgn2_6/ptodata/1/pna/US6059_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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		10. Appl			5782, A	84	,	37, Appl	37, Appl	981, App	981, App	7241, Ap	4171, Ap	80/52, A	15142, A	15144, A	· ~		_	٠.	1974, Ap	09	ັດ	942,	30,	3351,	3327,	3365,	277,	3925	677,	23	1710		3214	8399		1, Appli	52, Appl	52,	00	0	200, App	$\sim$	36271, A
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SOUTHFRIES	ID	US-09-048-911-10	-09-896-888-1	-09-896-888	-US01-	-US01-08631-2840	-US00-00903-3	-09-618-150-3	-09-985-153-3	S-10-100-683-	S-11-001-793-98	-10-198-846-72	0-198-846-4171	, ,	4-353-1314 4-2537-131	305R-1314	4-306B-208	7-632-20	7-632-208	08656-197	3-573-197	-08631-1336	-US01-08631-13	-US01-0	37-963-88	-08631-1	-08631-23	-08631-1336	-US02-39555A-227	37-963-39	-08631-567	-08631-5236	-08631-217	877-178	77-408-3214	I-USUI-08631-28	38-221-804-1	-08-443-781-1	3-09-426-293A-5	S-09-426-29	08-123-456-200	9-297-477	-09-994-404-200	-09-785-276A-3	US-10-357-930-36271
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Gaps Gaps ; 0 .. 0 20 20 20 1 ACTTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 50 ; FEATURE: ; OTHER INFORMATION: Description of Artificial Sequence: Primer US-09-048-911-10 ; OTHER INFORMATION: Description of Artificial Sequence: Primer US-09-896-888-10 1 ACTTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 1 ACTITAAGCTITATAGCGAIGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG Query Match 100.0%; Score 50; DB 16; Length 50; Best Local Similarity 100.0%; Pred. No. 2.9e-10; Matches 50; Conservative 0; Mismatches 0; Indels Length 50; Indels 100.0%; Score 50; DB 38; 100.0%; Pred. No. 2.9e-10; rative 0; Mismatches 0; US-09-048-911-10

Sequence 10, Application US/09048911

GENERAL INFORMATION:
TITLE OF INVENTION: Insect Expression Vectors
FILE REFERENCE: 80021-44

CURRENT APPLICATION NUMBER: US/09/048,911

CURRENT APPLICATION NUMBER: US 60/049,946

EARLIER APPLICATION NUMBER: US 60/049,946

EARLIER PILING DATE: 1997-03-27

NUMBER OF SEQ ID NOS: 50

SEQ ID NO 10

SEQ ID NO 10

LENGTH: 50 US-09-896-888A-10
; Sequence 10, Application US/09896888A
; GENERAL INFORMATION:
 APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Insect Expression Vectors
FILE REFERENCE: 80021-44
; CURRENT APPLICATION NUMBER: US/09/896,888A
; CURRENT APPLICATION NUMBER: US/09/048,911
PRIOR PILING DATE: 1998-03-26 APPLICANT: The University of British Columbia TITLE OF INVENTION: Insect Expression Vectors FILE REFERENCE: 80021-44 CURRENT APPLICATION NUMBER: US/09/896,888
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 09/048,911
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1997-03-27
NUMBER OF SEQ ID NOS: 50
SEQ ID NO 10 Sequence 10, Application US/09896888 GENERAL INFORMATION: TYPE: DNA ORGANISM: Artificial Sequence TYPE: DNA ORGANISM: Artificial Sequence FEATURE: Conservative Query Match Best Local Similarity Matches 50; Conserv US-09-896-888-10 ò g g ઠે

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NAME/KEY: SIMILAR

CCATION: (961).. (899)

COTHER INFORMATION: 100% homologous to Cloning vector pBACe3.6

OTHER INFORMATION: 1evansucrase, accession number U80929, Smith-Waterman Score=110.

NAME/KEY: misc_feature

LOCATION: (1)...(20795)

COTHER INFORMATION: n = a,t,c or g

PCT-US01-08631-28400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CT-US00-00903-37/c
Sequence 37, Application PC/TUS0000903
GENERAL INFORMATION:
APPLICANT: Human Secreted Proteins
TITLE OP INVENTION: 33 Human Secreted Proteins
FILE REFERENCE: PZ036.PCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: PCT/USOO/00903
CURRENT FILING DATE: 2000-01-18
EARLIER APPLICATION NUMBER: 60/116,330
EARLIER FILING DATE: 1999-01-19
NUMBER OF SEQ ID NOS: 144
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 37
LENGTH: 745
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NAME/KEY: SITE
COCATION: (48)
OTHER INFORMATION: n equals a, t, g,
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OTHER INFORMATION: n equals a,t,g,
PRATURE:
DAME/KEY: SITE
LOCATION: (27)
OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n equals a,t,g,
PEATURE:
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         TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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LOCATION: (739)
OTHER INFORMATION: n
FEATURE:
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LOCATION: (93)
OTHER INFORMATION:
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LOCATION: (745)
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LOCATION: (304)..(1047)
OTHER INFORMATION: 99% homologous to Cloning vector pBACe3.6
OTHER INFORMATION: levansucrase, accession number U80929, Smith-Waterman Score=1333.
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                                                                                                                                                                                                                                                                                                                                                                                                                  1 ACTTAAGCTTATAGCGATGACTGCCCCCTTTCCAGTCGGGAAACCTGTCG 50
                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Artificial Sequence: Primer US-09-896-888A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 72.0%; Score 36; DB 1; Length 16091; Best Local Similarity 88.6%; Pred. No. 0.00073; Matches 39; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                       Query Match
100.0%; Score 50; DB 38; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
Matches 50; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hyeeq, Inc.
ITILE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REPERENCE: 2127-2049
FILE REPERENCE: 2202-049
CURRENT APPLICATION NUMBER: 905540,217
FRIOR PILING DATE: 2001-03-30
PRIOR PILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-03-31
SROR APPLICATION NUMBER: 09/649,167
PRIOR PILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 25782
LENGTH: 16091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCT-US01-08631-28400

Sequence 28400, Application PC/TUS0108631

GENERAL INFORMATION:

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

FILE REPERENCE: 21272-049

CURRENT APPLICATION NUMBER: PCT/US01/08631

CURRENT APPLICATION NUMBER: 09/540,217

PRIOR PILING DATE: 2000-03-31

PRIOR PILING DATE: 2000-03-31

PRIOR FILING DATE: 2000-08-23

NUMBER OF SEQ ID NOS: 60736

SEQ ID NO 28400

LENGTH: 20795
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
PCT-US01-08631-25782/c
Sequence 25782, Application PC/TUS0108631
GENERAL INFORMATION:
PRIOR APPLICATION NUMBER: 60/049,946
PRIOR FILING DATE: 1997-03-27
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 10
LENGTH: 50
                                                                                                                                                 TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
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                                                                                                                                                                                                   PEATURE:
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NAME/KEY: SITE
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                                                                                                                                                    3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 50
                                                  Score 35.8; DB 1; Length 745; Pred. No. 0.00049; 0; Mismatches 8; Indels C
                                                                                                                               3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 50
                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: 33 Human Secreted Proteins
TITLE OF INVENTION: 33 Human Secreted Proteins
FILE REFERENCE: PRO36F1
CURRENT APPLICATION NUMBER: US/09/618,150
CURRENT FILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: 60/116,330
PRIOR FILING DATE: 1999-01-19
PRIOR FILING DATE: 1999-01-19
NUMBER OF SEQ ID NOS: 147
SOFFWARE: Patentin Ver. 2.0
SEQ ID NO 37
LENGTH: 745
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; OTHER INFORMATION: n equals a,t,g, or PCT-US00-00903-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                      Sequence 37, Application US/09618150
GENERAL INFORMATION:
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OTHER INFORMATION: n equals a,t,g,
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                                                      71.68;
83.38;
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                                                                                            40; Conservative
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ORGANISM: Homo sapiens
                                                                     Best Local Similarity
Matches 40; Conserv
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LOCATION: (739)
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US-09-618-150-37/c
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83.3%; Pred. No. 0.00049;
tive 0; Mismatches 8;
APPLICANT: Rosen et al.
TITLE OF INVENTION: 33 Human Secreted Proteins
FILE REFRENCE: P2036P1
CURRENT APPLICATION NUMBER: US/09/985,153
CURRENT PILING DATE: 2001-11-01
PRIOR PILING DATE: 2000-07-17
PRIOR APPLICATION NUMBER: PCT/US00/00903
PRIOR FILING DATE: 2000-07-17
PRIOR PILING DATE: 1099-01-19
PRIOR FILING DATE: 1999-01-19
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PATENTIN OFF: 2.0
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CURRENT FILING DATE: 2002-03-19
PRIOR APPLICATION NUMBER: US 60/040,162
PRIOR PILING DATE: 1997-03-07
PRIOR APPLICATION NUMBER: US 60/043,576
PRIOR APPLICATION NUMBER: US 60/047,601
PRIOR APPLICATION NUMBER: US 60/047,601
PRIOR PLING DATE: 1997-05-23
PRIOR PLING DATE: 1997-05-23
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TITLE OF INVENTION: Human Secreted Proteins
FILE REFERENCE: PS900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: n equals a,t,g, or c US-09-985-153-37
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OTHER INFORMATION: n equals a,t,g, or
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OTHER INFORMATION: n equals a,t,g,
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Best Local Similarity
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US-10-100-683-981/c
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; Sequence 37, Application US/09985153

RESULT 8 US-09-985-153-37/C

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CURRENT FILING DATE: 2004-12-02
PRIOR FLILING DATE: 2004-12-02
PRIOR FLILING DATE: 2004-12-02
PRIOR FLILING DATE: 2005-13-19
PRIOR FLILING DATE: 1997-03-19
PRIOR PLILING DATE: 1997-03-07
PRIOR PLILING DATE: 1997-03-07
PRIOR PLILING DATE: 1997-04-11
PRIOR FLILING DATE: 1997-04-11
PRIOR FLILING DATE: 1997-04-11
PRIOR PLILING DATE: 1997-06-23
PRIOR PLILING DATE: 1997-06-23
PRIOR PLILING DATE: 1997-06-23
PRIOR PLILING DATE: 1997-06-23
PRIOR PLILING DATE: 1997-04-11
PRIOR PLILING DATE: 1997-04-11
PRIOR PLILING DATE: 1997-06-23
PRIOR PLING DATE: 1997-06-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature; LOCATION: (745)...(745)
; COTHER INFORMATION: n equals a,t,g, or c
US-11-001-793-981
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LOCATION: (727)..(727)
OTHER INFORMATION: n equals a,t,g, or
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NAME/KEX: misc_feature
LOCATION: (739)..(739)
OTHER INFORMATION: n equals a,t,g, or
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OTHER INFORMATION: n equals a,t,g, or
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LOCATION: (93)...(93)
OTHER INFORWATION: n equals a,t,g,
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LOCATION: (27)...(27)
OTHER INFORMATION: n equals a,t,g,
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NAME/KEY: misc_feature
LOCATION: (48)...(48)
OTHER INFORMATION: n equals a,t,g,
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LOCATION: (163)..(163)
OTHER INFORMATION: n equals a,t,g,
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                    Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 13468 SOFTWARE: PatentIn Ver. 2.0
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PRIOR FILING DATE: 1997-08-22
PRIOR APPLICATION NUMBER: US 60/043,580
PRIOR FILING DATE: 1997-04-11
PRIOR FILING DATE: 1997-04-11
PRIOR PELICATION NUMBER: US 60/047,599
PRIOR PELICATION NUMBER: US 60/056,664
PRIOR APPLICATION NUMBER: US 60/056,664
PRIOR APPLICATION NUMBER: US 60/043,314
PRIOR PELING DATE: 1997-04-11
PRIOR PELING DATE: 1997-05-23
PRIOR APPLICATION NUMBER: US 60/047,632
PRIOR APPLICATION NUMBER: US 60/056,892
PRIOR FILING DATE: 1997-05-23
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; Sequence 981, Application US/11001793
; GENERAL INFORMATION:
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LOCATION: (745)...(745)
OTHER INFORMATION: n equals a,t,g,
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LOCATION: (3). 7(3)
OTHER INFORMATION: n equals a,t,g,
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LOCATION: (48)..(48)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RATURE:
NAME/KEY: misc_feature
LOCATION: (113).
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (163)...(163)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (27) ... (27)
OTHER INFORMATION: n equals a,t,9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (727)..(727)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: misc_feature
LOCATION: (739). (739)
OTHER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COCATION: (93)...(93)
THER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-100-683-981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 981
LENGTH: 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
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; TYPE: DNA
; ORGANISM: Homo s
US-09-814-353-13142
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US-09-814-353-13142
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                                                                                                                                                                        APPLICANT: Lillie, James
APPLICANT: Lillie, Yongyao
APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhan
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENT FILING DATE: 2002-07-18
FRIOR APPLICATION NUMBER: 60/306,220
FRIOR APPLICATION NUMBER: 60/306,220
FRIOR APPLICATION NUMBER: 60/306,220
FRIOR PILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTWARE: FESTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: misc_feature
; LOCATION: 282, 300, 554, 592, 650, 707, 720, 728, 755, 767, 775, 791
; CTHER INFORMATION: n = A,T,C or G
US-10-198-846-7241
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: LOCATION: 2, 3, 4, 6, 9, 10, 11, 531, 585, 667, 691, 696, 732, 742,

: LOCATION: 763, 764, 780, 816, 841, 856

: OTHER INFORMATION: n = A,T,C or G
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168 rraarngcgrrdcgcrcacrccccccrrrccacrccccaaaccrcrcrc 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 71.6%; Score 35.8; DB 49; Length 791; Best Local Similarity 83.3%; Pred. No. 0.0005; Matches 40; Conservative 0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 544 TTAATTGCGTNGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71.6%; Score 35.8; DB 49; Length 869; 83.3%; Pred. No. 0.00051; tive 0; Mismatches 8; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Geguence 4171, Application US/10198846

GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Mullie, James
APPLICANT: Wang, Youzhen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: NOVEL GENES, CAMERY PRE
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILE REFERENCE: MRI-049
CURRENY APPLICATION NUMBER: US/10/198,846
CURRENY FILING DATE: 2002-07-18
PRIOR FILING DATE: 2001-07-18
PRIOR FILING DATE: 2001-07-18
PRIOR FILING DATE: 2001-07-18
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4171
LENGTH: 869
                                                                                                                         Sequence 7241, Application US/10198846 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
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Matches 40; Conserv
                                                                                                    US-10-198-846-7241
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US-10-198-846-417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 7241
LENGTH: 791
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WESULT 13
US-10-437-963-80752/C
Sequence 80752, Application US/10437963
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Exer, You, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Boukharov, Andrey A.
APPLICANT: Buckharov, Brad
APPLICANT: Buckharov, Brad
APPLICANT: Buckharov, Andrey A.
APPLICANT: Buckharov, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 80752
LENGTH: 415
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Sequence 13142, Application US/09814353

GENERAL INFORMATION:

APPLICANT: Lee, John
APPLICANT: Lilie, James

TITLE OF INVENTION: NOWEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: NOWEL GENES, COMPOSITIONS, KITS, AND METHODS FOR TITLE OF INVENTION: THERAPY OF OVARIAN CANCER

TITLE OF INVENTION: THERAPY CANCER

TITLE OF INVENTION: THERAPY 2001-02.1

PRICA FILING DATE: 2000-03-21

PRICA PELICATION NUMBER: US 60/191,031

PRICA FILING DATE: 2000-05-25

PRICA PELICATION NUMBER: US 60/210,940

PRICA APPLICATION NUMBER: US 60/210,661

PRICA APPLICATION NUMBER: US 60/250,661

PRICA APPLICATION NUMBER: US 60/250,661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                 569 Traatrgcgfrgcgcrnacrgcccgcrrrccagrcggaaaccrgrcg 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ACTTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
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; OTHER INFORMATION: Clone ID: PAT_MRT4530_80346C.1
US-10-437-963-80752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 71.2%; Score 35.6; DB 54
Best Local Similarity 82.0%; Pred. No. 0.00054;
Matches 41; Conservative 0; Mismatches 9
TTAAGCTTATAGCGATGACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Oryza sativa
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                                                                                                                                                                                                                                                                                   Sequence 13142, Application US/09814353A

Sequence 13142, Application US/09814353A

GENERAL INFORMATION:
APPLICANT: Let, John
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-006B

CURRENT PELING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: US 60/191,031

PRIOR APPLICATION NUMBER: US 60/207,124

PRIOR APPLICATION NUMBER: US 60/207,124

PRIOR PLING DATE: 2000-05-25

PRIOR PLING DATE: 2000-06-15

PRIOR PLING DATE: 2000-06-15

PRIOR PLING DATE: 2000-07-07

PRIOR FILING DATE: 2000-07-07

PRIOR FILING DATE: 2000-07-07

PRIOR PLING DATE: 2000-07-25

PRIOR PLING DATE: 2000-07-25

PRIOR PLING DATE: 2000-07-25

PRIOR PRIOR APPLICATION NUMBER: US 60/257,672

PRIOR PLING DATE: 2000-07-25

PRIOR PRIOR APPLICATION NUMBER: US 60/257,672
                                                          Gaps
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                                                                                                                                                        516 ATTTAATTGCGTTGCGTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 565
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0
                                                                                                            1 ACTIVAGGITATAGGGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 50
Score 35.6; DB 35; Length 586;
Pred. No. 0.00057;
0; Mismatches 9; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 35.6; DB 35; Length 586; Pred. No. 0.00057;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13142
LENGTH: 586
Query Match
Best Local Similarity 82.0%;
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 82.0
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
CORGANISM: Homo sapiens
US-09-814-353A-13142
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516 ATTTAATTGCGTTGCGCTCACTGCCCCTTTCCAGTCGGGAAACCTGTCG 565

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Search completed: May 10, 2005, 09:18:57 Job time : 414.906 secs

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May 10, 2005, 05:51:35 ; Search time 123.262 Seconds (without alignments) 834.449 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pna/PCT NEW COMB.seq:*

2: /cgn2_6/ptodata/1/pna/PCT NEW COMB.seq:*

3: /cgn2_6/ptodata/1/pna/USO6 NEW COMB.seq:*

4: /cgn2_6/ptodata/1/pna/USO7 NEW COMB.seq:*

5: /cgn2_6/ptodata/1/pna/USO9 NEW COMB.seq:*

6: /cgn2_6/ptodata/1/pna/USO9 NEW COMB.seq:*

7: /cgn2_6/ptodata/1/pna/USO9 NEW COMB.seq:*

8: /cgn2_6/ptodata/1/pna/USO1 NEW COMB.seq:*

9: /cgn2_6/ptodata/1/pna/USO1 NEW COMB.seq:*

10: /cgn2_6/ptodata/1/pna/USO1 NEW COMB.seq:*

11: /cgn2_6/ptodata/1/pna/USO1 NEW COMB.seq:*

12: /cgn2_6/ptodata/1/pna/USO1 NEW COMB.seq:*

12: /cgn2_6/ptodata/1/pna/USO1 NEW COMB.seq:*

12: /cgn2_6/ptodata/1/pna/USO1 NEW COMB.seq:*

13: /cgn2_6/ptodata/1/pna/USO1 NEW COMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                     nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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50
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Seguence 102508,	Sequence 25782, A	Sequence 28400, A	Sequence 13360, A	Sequence 13349, A	Sequence 4942, Ap	Sequence 13351, A	Sequence 23327, A	Sequence 13365, A	Sequence 5677, Ap	Sequence 5236, Ap	Seguence 21710, A	Sequence 28399, A	Sequence 7, Appli	Sequence 21773, A	Sequence 1746, Ap	Sequence 1748, Ap	Sequence 6994, Ap	Sequence 10137, A	Sequence 20, Appl
	Des	Š	Š	Š	Š	Š	Š	Š	ത്	മ്	Š	ၓ	Š	Š	0,	Š	ഗ്	Š	Š	ഗ്	Š
SUMMARIES	ai	US-10-703-032-102508	US-10-450-763-25782	US-10-450-763-28400	US-10-450-763-13360	US-10-450-763-13349	US-10-450-763-4942	US-10-450-763-13351	US-10-450-763-23327	US-10-450-763-13365	US-10-450-763-5677	US-10-450-763-5236	US-10-450-763-21710	US-10-450-763-28399	1 US-11-035-627-7	US-10-450-763-21773	US-10-472-963-1746	US-10-472-963-1748	US-10-450-763-6994	US-10-450-763-10137	US-10-841-603B-20
	E DB	0	Φ.	œ	æ	<b>c</b> o	œ		<b>60</b>	œ _	80	œ _	ω.	80	Η.	ω	9	9	œ _	œ _	6
	Length	451	16091	20795	1637	1695	1942	2346	2424	2710	2757	5909	10771	20974	271	282	364	364	389	389	395
	% Query Match	73.6	72.0	72.0	71.2	71.2	71.2	71.2	71.2	71.2	71.2	71.2	71.2	71.2	70.4	70.4	70.4	70.4	70.4	70.4	70.4
	Score	36.8	36	36	35.6	35.6	35.6	35.6	35.6	35.6	35:6	35.6	35.6	35.6	35.2	35.2	35.2	35.2	35.2	35.2	35.2
	Result No.	1	70 ن	m	Ω 4	υ N	9	7	<b>8</b> 0	٥ د	c 10	c 11	c 12	c 13	c 14	c 15	c 16	c 17	c 18	c 19	20

Sequence 2514, Ap Sequence 2518, Ap Sequence 428, App Sequence 55, Appl Sequence 10251, Sequence 10251, Sequence 11803, A Sequence 11803, A Sequence 12, Appl Sequence 12, Appl Sequence 1156, Ap Sequence 1147, App Sequence 251, Ap Sequence 10316, A Sequence 2830, A Sequence 28330,	p,	Length 451; Indels 0; Gaps 0;
US-11-090-997-2544 US-10-090-997-2578 US-10-10-990-997-2578 US-10-10-10-991-997-2578 US-10-10-10-991-997-2578 US-10-10-10-10-10-10-10-10-10-10-10-10-10-	ALIGNMENTS  S/10703032  s/10/703,032  06 020,338  PAT_TA_102508	Score 36.8; DB 9; L Pred. No. 8e-06; 0; Mismatches 7;
35.2 70.4 421 10 35.2 70.4 456 10 35.2 70.4 456 10 35.2 70.4 456 10 35.2 70.4 508 2 35.2 70.4 508 2 35.2 70.4 508 2 35.2 70.4 508 8 35.2 70.4 508 8 35.2 70.4 656 13 35.2 70.4 656 13 35.2 70.4 666 9 35.2 70.4 666 9 35.2 70.4 666 9 35.2 70.4 668 9 35.2 70.4 686 9 35.2 70.4 686 9 35.2 70.4 686 9 35.2 70.4 686 9 35.2 70.4 686 9 35.2 70.4 686 9 35.2 70.4 70.5 2 35.2 70.4 70.5 2	-102508 2508, Applicatio ORMATION: Kovalic, David Byrum, Joseph Conner, Timcth Conner, Timcth Conner, Yndwei Asucci, James Zhou, Yibua NVENTION: Nuclei NVENTION: Nuclei NVENTION: NUMBER: 2001-12 SEQ ID NOS: 2111 02508 Triticum aestiv ORMATION: Clone	Query Match 73.6%; Best Local Similarity 85.4%; Matches 41; Conservative
0 0 0 0 0 0 0 1 0 1 0 1 0 0 0 0 0 0 0 0	RESULT 1 US-10-703-032 Sequence 10 GENERAL INF APPLICANT: APPLICAN	Query Match Best Local Matches 4

94 TTAATTTCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 141 RESULT 2
US-10-450-763-25782, Application US/10450763
; Sequence 25782, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TILLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US 3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGT 임 ò

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NAME/KEY: SIMILAR
LOCATION: (85)...(1912)
OTHER INFORMATION: 97% homologous to Homo sapiens putative p150, accession number
OTHER INFORMATION: U93563, Smith-Waterman Score=3485.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: SIMILAR
LOCATION: (241)
OTHER INFORMATION: 100% homologous to Homo sapiens endoglycan, accession number
OTHER INFORMATION: AF219137, Smith-Waterman Score=1070.
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                                                 APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REPERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: 00/540,217
PRIOR PILING DATE: 2001-03-30
PRIOR PLING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUSTOM
SEQ ID NOS: 60736
LENGTH: 1637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REPERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR PILING DATE: 2001-03-30
PRIOR FILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-03-31
PRIOR PILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SEQ ID NO 13349
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Pred. No. 3.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 71.2%; Score 35.6; DB 8; Best Local Similarity 82.0%; Pred. No. 3.3e-05; Matches 41; Conservative 0; Mismatches 9;
    Sequence 13360, Application US/10450763 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-450-763-13349/c;
Sequence 13349, Application US/10450763
; GENERAL INFORMATION:
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i_LOCATION: (1)...(1637)
/ CTHER INFORMATION: n = a,t,c or g
US-10-450-763-13360
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82.0%;
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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OTHER INFORMATION: 99% homologous to Cloning vector pBACe3.6

OTHER INFORMATION: levansucrase,accession number U80929,Smith-Waterman Score=1333.
US-10-450-763-25782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: SIMILAR
LOCATION: (961)...(899)
OTHER INFORMATION: 100% homologous to Cloning vector pBACe3.6
OTHER INFORMATION: levansucrase, accession number U80929, Smith-Waterman Score=110.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36; DB 8; Length 20795;
Pred. No. 3.7e-05;
0; Mismatches 5; Indels
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CTP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 28400
LUMBETH OF SEQ ID NOS: 60736
SEQ ID NO 28400
LUMBETH OF SEQ ID NOS: 60736
SEQ ID NO 28400
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CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR FILING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
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; Sequence 28400, Application US/10450763
; GENERAL INFORMATION:
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; OTHER INFORMATION: n = a,t,c or g
US-10-450-763-28400
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Best Local Similarity 88.6%;
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
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US-10-450-763-13360/c
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                                                                                                                                                                                                                                                    SEQ ID NO 25782
LENGTH: 16091
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Gaps

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Indels

82.0%; Pred. No. 3.6e-05; tive 0; Mismatches 9;

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Best Local Similarity 82.0
Matches 41; Conservative
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NAME/KEY: SIMILAR
LOCATION: (1801).
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OTHER INFORMATION: 97% homologous to Homo sapiens putative p150, accession number OTHER INFORMATION: U93568, Smith-Waterman Score=3707.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (1514)..(1942)
OTHER INFORMATION: 100% homologous to Cloning vector pSacBII SacB, accession OTHER INFORMATION: number U09128, Smith-Waterman Score=768.
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                                                                                    651 AATTAATTGCGTTGCGCTCACTGCCGCTTTCCAGTCGGGAAACCTGTCG 602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13351, Application US/10450763
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT APPLICATION NUMBER: PCT/US01/08631
PRIOR PILING DATE: 2001-03-30
PRIOR PLING DATE: 2001-03-30
PRIOR PLING DATE: 2000-03-31
PRIOR PLING DATE: 2000-03-31
PRIOR PLING DATE: 2000-03-31
PRIOR PLING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
                                                                                                                                                                                                                                       APPLICANT: Hyseq, inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790C113/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR PILING DATE: 2001-03-30
PRIOR PILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 60736
9; Indels
0; Mismatches
                                          1 ACTTAAGCTTATAGCGATGACTGCCCGCT
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US-10-450-763-4942/c
; Sequence 4942, Application US/10450763
; GENERAL INFORMATION:
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Best Local Similarity 82.00
Thes 41; Conservative
41; Conservative
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ORGANISM: Homo sapiens
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LOCATION: (1514)...
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LENGTH: 2346
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LENGTH: 1942
Matches
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DB 8; Length 2346;

71.2%; Score 35.6;

Query Match

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FEATURE:
NAME/KEY: SIMILAR
LOCATION: (1)...(228)
OTHER INFORMATION: 94% homologous to Homo sapiens Alzheimer's disease protein
OTHER INFORMATION: encoded by DNA from plasmid pGCS2232, accession number W21578, Smith
OTHER INFORMATION: Waterman Score=392.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: 100% homologous to Homo sapiens A human proliferation and porter INFORMATION: apoptosis related protein, accession number Y84901, Smith-Waterman CHER INFORMATION: Score=838.
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                                                                 1672 AATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 1721
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1 ACTIVAGCTIVITACGATGACTGCCCCCTTICCAGTCGGGAAACCTGTCG
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                                                                                                                                                                                                                                                                                                   ATTILE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2000-06-11
PRIOR APPLICATION NUMBER: PCT/USO1/08631
PRIOR FILING DATE: 2000-03-30
PRIOR FILING DATE: 2000-03-31
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

FILE REFERENCE: 790CTP3/US

CURRENT APPLICATION NUMBER: US/10/450,763

PRIOR APPLICATION NUMBER: PCT/US01/08631

PRIOR APPLICATION NUMBER: PCT/US01/08631

PRIOR FILING DATE: 2000-03-10

PRIOR PILING DATE: 2000-03-31

PRIOR PILING DATE: 2000-03-31

PRIOR FILING DATE: 2000-08-23

NUMBER OF SEQ ID NOS: 60736

SOFTWARE: CUSTOM

LENGTH: 2710

LENGTH: 2710
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                                                                                                                                                                RESULT 8
US-10-450-763-23327/c
; Sequence 23327, Application US/10450763
; GENERAL INFORMATION:
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LOCATION: (1)..(840)
OTHER INFORMATION: 94% homologous to Cloning vector pZC320 SopA,accession number
OTHER INFORMATION: UZ6464,Smith-Waterman Score=1403.
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71.2%; Score 35.6; DB 8; Length 10771;
Best Local Similarity 82.0%; Pred. No. 4.8e-05;
Matches 41; Conservative 0; Mismatches 9; Indels 0;
                                                                              Length 5909;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ACTIVAGGETATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
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; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.; TILE OF INVENTION:
; TILE REPERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR PILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR PILING DATE: 2000-08-23
                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REPRENCE: 790C1P3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
; OTHER INFORMATION: number U26464, Smith-Waterman Score=1509.
US-10-450-763-5236
                                                                                                                             Indels
                                                                         Score 35.6; DB 8;
Pred. No. 4.3e-05;
0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                  US-10-450-763-21710/c
; Sequence 21710, Application US/10450763
; GENERAL INFORMATION:
                                                                                                                                                                                  1 ACTIAAGCTTATAGCGATGACTGCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:

NAME/KEY: misc feature
LOCATION: (1)...(10771)

OTHER INFORMATION: n = a,t,c or g
US-10-450-763-21710
                                                                            Query Match 71.2%;
Best Local Similarity 82.0%;
Matches 41; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-450-763-28399/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Custom
SEQ ID NO 21710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Custo
SEQ ID NO 28399
LENGTH: 20974
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CHER INFORMATION: 50% homologous to Cloning vector pZC320 SopA, accession number: OTHER INFORMATION: U26464, Smith-Waterman Score=40.
US-10-450-763-5677
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LOCATION: (5001)..(5864)
OTHER INFORMATION: 100% homologous to Cloning vector pZC320 SopA,accession
                                                                                                           Gaps
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                                                                                                                                                                                       1080 ATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGAAACCTGTCG 1031
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                                                 71.2%; Score 35.6; DB 8; Length 2710; 82.0%; Pred. No. 3.7e-05; ive 0; Mismatches 9; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2757;
                                                                                                                                                        1 ACTTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
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                                                                                                                                                                                                                                                                                                                     Sequence 5677, Application US/10450763
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TILLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: PCT/US01/08631
PRIOR APPLICATION NUMBER: 09/540,217
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-03-31
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SEQ ID NOS: 60736
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR PLILING DATE: 2001-03-30
PRIOR PLILING DATE: 2000-03-31
PRIOR PLILING DATE: 2000-03-31
PRIOR PLILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: CUSTOM
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Pred. No. 3.7e-05;
0; Mismatches 9;
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71.2%;
Best Local Similarity 82.0%;
Matches 41; Conservative (
                                                                                                        41; Conservative
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ORGANISM: Homo sapiens
                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                   RESULT 10
US-10-450-763-5677/c
     US-10-450-763-13365
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                                                       Query Match
                                                                                                        Matches
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APPLICANT: University of North Carolina at Chapel Hill
APPLICANT: Wilson, W. David
APPLICANT: Boykin, David W
APPLICANT: Tidwell, Richard R
TITLE OF INVENTION: NOVEL COMPOUNDS THAT EXHIBIT SPECIFIC MOLECULAR RECOGNITION OF
TITLE OF INVENTION: MIXED NUCLEIC ACID SEQUENCES AND BIND IN THE DNA MINOR GROOVE AS
TITLE OF INVENTION: MIXED NUCLEIC ACID SEQUENCES AND BIND IN THE DNA MINOR GROOVE AS
TITLE OF INVENTION: MIMER: US/11/035,627
CURRENT APPLICATION NUMBER: US 10/653,677
FRIOR APPLICATION NUMBER: US 09/745,004
PRIOR FILING DATE: 2000-12-29
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 7
LENGTH: 271
LENGTH: 271
                                              NAME/KEY: SIMILAR
LOCATION: (7)..(387)
OTHER INFORMATION: 100% homologous to Bacillus amyloliquefaciens precursor (AA ·
OTHER INFORMATION: 29 to 443), accession number X52988, Smith-Waterman Score=664.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: BCrRi-PvulI fragment from plasmid pBS+, antisense strand
US-11-035-627-7
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                                                                                                                                                                                                                                                                                                                              Query Match 71.2%; Score 35.6; DB 8; Length 20974; Best Local Similarity 82.0%; Pred. No. 5.5e-05; Matches 41; Conservative 0; Mismatches 9; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35.2; DB 11; Length 271; Pred. No. 3.5e-05; 0; Mismatches 8; Indels 0
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US-10-450-763-21773/C
; Sequence 21773, Application US/10450763
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; FRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR PLILING DATE: 2001-03-30
; PRIOR FILING DATE: 2001-03-30
; PRIOR FILING DATE: 2000-03-31
                                                                                                                                                            FEATURE:

NAME/KEY: misc_feature

LOCATION: (1)...(20974)

OTHER INFORMATION: n = a,t,c or g
US-10-450-763-28399
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70.4%;
Best Local Similarity 83.3%;
Matches 40; Conservative (
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial
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FEATURE:
| NAME/KEY: SIMILAR
| LOCATION: (243)..(214)
| OTHER INFORMATION: 100% homologous to Homo sapiens Amino acid sequence of a
| OTHER INFORMATION: human secreted peptide, accession number Y10930, Smith-Waterman Scory OTHER INFORMATION: =66.
| US-10-450-763-21773
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                                                                                                                                                                                                                                                                                                                                                                             Length 282;
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Pred. No. 3.5e-05;
0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: May 10, 2005, 09:51:26 Job time : 123.262 secs
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SOFTWARE: Custom
SEQ ID NO 21773
LENGTH: 282
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 83.3%;
Matches 40; Conservative
                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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BJ668962 BJ668962 AU069599 AU069599 BPB94955 BPB74955 BJ671717 BJ6771717 BJ6907999 QU022D02 O BM419997 R020C12 O CB865576 HD10A15w AG060720 Pan trog1 AG14861 Pan trog1 AG14861 Pan trog1 AJ57743 Arabidops CF56104 79225 S'U B1977595 dd94b01.Y B1977955 BN TP-E5-a AG10915 Pan trog1 AG108621 Pan trog1 AG04821 Pan trog1 AG04821 Pan trog1 CC96240 ISBN-2713 AG041822 CTT-HSP-2 CC961712 BOIDV76TF

ritle:
Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Minimum DB e Maximum DB e

Database

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Direct Submission
Submitted (01-OCT-2001) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
2 (bases 1 to 412)
Roth.C.W., Bery.P.T., Ke,Z. and Collins,P.H.
Submitted (01-OCT-2001) BBMI, Institut Pasteur, 25, rue du Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CNS07H0H
Anopheles gambiae GSS T7 end of clone 23P13 of library NotreDamel from strain PEST of Anopheles gambiae (African malaria mosquito),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Roux, Paris 75015, France
This clone is from an A. gambiae BAC library provided by F.H.
Collins and sequenced Genoscope in collaboration with the
Laboratory of Biochem. and Biol. Molec. of Insects, Institut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  152 TTAATTTTTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 199
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Anopheles gambiae
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/organism="Anopheles gambiae"
/organism="Anopheles gambiae"
/mol_type="genomic DNA"
/strain="pEST"
/db_xref="taxon:7165"
/clone="23P13"
/clone=1ib="NotreDamel"
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Pred. No. 0.00023;
0; Mismatches 6
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                                                                                                                                                                                                                                        AG134861
ATH517143
CF569104
                                                                     BP874955
BJ671717
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AG060720
AG043113
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AG109195
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CL096240
AQ041632
CC961712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genomic survey sequence.
AL610451
AL610451.1 GI:15916636
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llarity 87.5%;
Conservative
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Best Local Similarity
Matches 42; Conserv
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Genoscope
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\begin{smallmatrix} \mathbf{G} & \mathbf{G} 
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1
CNSO7HOH
LOCUS
DEFINITION
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AUTHORS
TITLE
JOURNAL
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AUTHORS
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JOURNAL
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CIT-HSP-2
UMC-pd3ov
UMC-pd8mm2
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AU069015 AU069015
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                                                                                                                                                            May 10, 2005, 03:45:00 ; Search time 350.316 Seconds (without alignments) 5432.847 Million cell updates/sec
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AL610727
C0048749
AG068743
AG125607
AG125607
AG118925
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AG102051
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                       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                     nucleic search, using sw model
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AQ076114
CO990192
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CO954011
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BH243517
AU069015
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Gapop 10.0 , Gapext 1.0
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seq length: 2000000000
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Match Length DB
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9b est6: *
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Büteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1. (Dasse 1 to 125)
Berry, K., Granger, D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready Map Building
Unpublished (1998)
Unpublished (1998)
Unpublished (1998)
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             174 bp DNA linear GSS 20-AUG-1998 CIT-HSP-2364K4.TF CIT-HSP Homo sapiens genomic clone 2364K4, Genomic survey sequence. AQ076128 GSS 20-AUG-1998 GSS. CIT-HSP Homo sapiens genomic clone 2364K4, AQ076128 GSS.
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                                                     AQ080570 125 bp DNA linear GSS 20-AUG-1998 CIT-HSP-2358M2.TF CIT-HSP Homo sapiens genomic clone 2358M2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
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1 (Dassel 1 to 174)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Venter, J.C., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
Use of a random human BAC End Sequence Database for Sequence-Ready
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Seg primer: M13-21
Class: BAC ends.
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/organism="Homo sapiens"
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                                                                                               genomic survey sequence
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Homo sapiens
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Best Local Similarity
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AQ076128
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                   RESULT 2
AQ080570
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TITLE

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Homo sapiens (human)

Homo sapiens (human)

Homo sapiens

Homo sapiens

Homo sapiens

Bukaryorta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 177)

Sadams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K.,

Barry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and

Venter, J.C.

Use of a random human BAC End Sequence Database for Sequence-Ready

Map Building

Unpublished (1998)

Contact: Mark Adams

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712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: madama@eligr.org

Clones are available from Research Genetics (info@resgen.com). BAC

Home are available from Research Genetics (info@resgen.com). Home and Search Pages.
Map Building
Unpublished (1998)
Contact: Mark Adams
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: madadams@digr.org
Enail: madams@digr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.iigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13-21
Class: BAC ends.
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Seg primer: Mi3-21
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Male"
/cell_type="Sperm"
/clone_lib="CIT-HSP"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII"
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Organism="Homo sapiens"

/mol_type="genomic DNA"

/db xref="taxon:9606"

/clone="2364M4"
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/clone="2364K4"
                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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AQ076155.1 GI:3436289
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scrofa cDNA 3', mRNA sequence.
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CO990192
LOCUS CO990192 372 bp mRNA linear BST 09-SEP-2004.
DEFINITION UMC-pd3ov2-002-g02 Oviduct gilt D3 of estrous cycle pd3ov Sus
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Unpublished (1998)
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Email: mdadams@tigr.org
Email: mdadams@tigr.org
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Adamm, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13-21
Class: BAC ends.
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/clone_lib="CIT-HSP"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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CIT-HSP-2368K7.TF CIT-HSP Homo sapiens genomic clone 2368K7,
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/clone_lib="CIT-HSP"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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                                                                                                                               Score 36.8; DB 8; Length 177;
Pred. No. 0.00086;
0; Mismatches 7; Indels (
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/db_xref="taxon:9606"
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                                                                                                                               73.6%;
ilarity 85.4%;
Conservative (
/sex="Male"
/cell type=
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                                                                          HindIII"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       end search page:
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Best Local Similarity
Matches 41; Conservat
                                                                                                                                                Similarity
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Venter, J.C.
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                                                                                                                               Query Match
Best Local (
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KEYWORDS
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http://genome.rnet.missouri.edu/Swine/Methods.html.
http://genome.rnet.missouri.edu/Swine/Methods.html.
Library Construction (Standard Protocol): All procedures
discussed in this section have been described in detail
elsewhere (Soares et al., 1994; Bonaldo et al., 1996;
Jiang et al., 2001). Total cellular RNA from each sample
was isolated by using STAT-60 reagent (Tel-Test,
Friendswood, TX) and poly(A) + RNA was obtained by two
rounds of purification with the Oligotex mRNA isolation
kit (Qiagen) according to the manufacturer's instructions.
The oviduct libraries and the Day 3, 6 and 10 endometrium
libraries were constructed essentially as described by the
manufacturer's instructions provided with the SuperScript
Plasmid System (Invitrogen, cat. no. 18248-013). Briefly,
Img of poly(A) + RNA will be annealed at 37 degrees Celsius with SuperScript
Plasmid System (Invitrogen, cat. no. 18248-013). Briefly,
Img of poly(A) + RNA will be annealed at 37 degrees (Jiang et al., 2001). The 'tag' represents a
transcriptuse (Jiang et al., 2001). The 'tag' represents a
tissue/stage-specific ten-base sequence identifier
(http://genome.ulowa.edu/pubsoft/software.html) present in
the oligonuclectide used to prime first-strand synthesis.
Second strand synthesis was performed with 74 bNA
polymerase in the presence of DNA ligase and RNase H.
After second strand synthesis, the double-stranded cDNAs
was ligated to Sall adapters (Invitrogen-Life
Technologies) and digested with NotI. The cDNAs will be
size selected by passage through cDNA size fractionation
columns (Invitrogen-Life technologies) The cDNAs exived
from each developmental steage of a particular tissue were
mixed on an equimolar basis and ligated directionally into
the NotI and Sall sites of the possage the prosents. the plasmids
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Woods, R.J., Spollen, W.G., Forrester, L.J., Mathialagan, N.,
Prather, R.S. and Green, J.A.
Large-scale Generation and Analysis of Expressed Sequence Tags from
Porcine endometrium and oviduct
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//clone lib="pd3ov"
/note="Vector: pSport1; Funding: A grant from the Monsanto Company to the University of Missouri. Genetic Source: Badometrium and oviduct tissues from various stages of the estrous cycle were collected from crossbred pigs (Sus scrofa domestica), frozen in liquid nitrogen immediately after collection, and stored at -80 degrees Celsius until RNA extraction. The specific tissues collected were Day 0 and Day 3 whole oviducts and Days 3, 6, 10 and 12-14 endometrium. More information regarding the methods can be
                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
"Labses 1 to 372)
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/db_xref="taxon:9823"
/dev_stage="Oviduct from a gilt on day 3 of the estrous
cycle"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2004)
Contact: DNA Core Facility (Swine Project)
Animal Science - RS Prather
University of Missouri-Columbia
M616 Medical Sciences Bldg., Columbia, M0 65212, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
CO990192.1 GI:51349466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: (573)882-0428
Fax: (573)884-5552
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                                                                                                  Sus scrofa (pig)
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(Invitrogen). After ligation of the inserts, the plasmids

source

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will be electroporated into DH10B bacteria. The day 12-14 endometrium library was synthesized by Dr. Bento Soares' laboractory (University of Iowa) and was cloned into the T3T7pac vector as described elsewhere (Bonaldo et al., 1996). Preliminary Library Characterization: Randomly chosen clones from each library were analyzed by restriction digestion to determine average insert size (96 clones) and by sequencing (-4 96 well plates) to confirm library quality [e.g. the presence of short polyA+ tails, genomic DNA contamination (must be <1%), ribosomal RNA clones (must be <1%), etc.] and to provide a sequence database representing the predominant clones in each library. The clones were sequenced at the University of Missouri-Columbia DNA Core Facility. Bioinformatics work was performed by GK Springer's bioinformatics group (WG Spollen, JE Ries, A Guillen, AA Khambati, RV Patel, CM Topinka, SB Bhuiyan) in Computer Science and Health Management and Informatics Departments at the University of Missouri-Columbia. Clone Requests: Requests for clones should be made to the Director of the University of Missouri DNA Core facility at: porcine@rnet.missouri.edu. Citations: 1. Bonaldo MF, Lennon G, Soares MB.
Normalization and Subtraction: TWo approaches to facility at: porcine@rnet.missouri.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     373 bp mRNA linear EST 09-SEP-2004 UMC-99mm2-002-g08 8mm ovarian follicle p8mm Sus scrofa cDNA 3', CO947892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jiang.H., Whitworth,K.M., Bivens,N.J., Ries,J.E., Woods,R.J.,
Forrester,L., Springer,G.K., Mathialagan,N., Agca,C.,
Prather,R.S. and Lucy,M.C.
Large-scale Generation and Analysis of Expressed Sequence Tags from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        facilitate gene discovery. Genome Ref. 1996; 6:791-806. 2. Janng H. Bivens NJ. Ries TB. Whitworth RW. Green JA. Forrester B. Springer GK. Didion BA. Mathialagan N. Prather RS. Lucy MC (2001) Constructing cDNA libraries
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Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus.
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Biotechniques 31:38-42. 3. Soares MB, MF Banaldo, P
Jelene, L Su, L Lawton, A Efstrantiadis. 1994.
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University of Missouri-Columbia
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(573)884-5552
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Unpublished (2004)
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Matches 41; Conserve
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POLYA=No.
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Sequencial rearrant series of the pubsoft/software. html) present in the oligonucleotide used to prime first-strand synthesis. Second strand synthesis was performed with T4 DNA polymerase in the presence of DNA ligase and RNAse H. After second strand synthesis, the double-stranded cDNAs was ligated to Sall adapters (Invitrogen-Life columns (Invitrogen-Life technologies). The cDNAs will be size selected by passage through cDNA size fractionation columns (Invitrogen-Life technologies). The cDNAs derived from each developmental stage of a particular tissue were mixed on an equimolar basis and ligated directionally into the NotI and Sall sites of the pSPORTI vector. (Invitrogen). After ligation of the inserts, the plasmids will be electroporated into DHAOB bacteria. Preliminary Library were analyzed by restriction digestion to determine average insert size (96 clones) and by sequencing (~4 96-well plates) to confirm library quality [e.g. the presence of short poly4+ tails, genomic DNA confamination (must be cl$), ribosomal RNA clones (must be cl$), etc.] and to provide a sequence database representing the predominant clones in each library. The clones were sequenced at the University of Missouri-Columbia DNA Core Facility, Bioinformatics work was performed by GK Springer's bioinformatics group (WG Spollen, JB Ries, A Guillen, AA Khambati, RV Patel, CM Topinka, SB Bhuiyan) in Computer Science and Health Management and Informatics Departments at the University of Missouri-Columbia. Clone Requests: Requests for clones should be made to the Director of the University of Missouri-Columbia. Clone Requests: Requests for clones should be made to the Director of the University of Missouri-Columbia. In Bonaldo MF Lennon G, Soares MB.

Citations: 1. Bonaldo MF Lennon G, Soares MB.

Normalization and Subraction: Two approaches to
                     /dev stage="8mm ovarian follicle"
/dow stage="8mm ovarian follicle"
/clone_lib="p8mm"
/clone_lib="p8mm"
/clone_lib="p8mm"
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/clone_lib="p8mm"
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/clone_lib="p8mm"
/clone ovary, dissected follicles, or corpora lutea) was collected from crossbred pigs (Suss scrofa domestica), frozen in liquid nitrogen shortly after collection, and stored at -80 degrees Celsius until RNA extraction. The tissue from several individual pigs was pooled for the purpose of RNA extraction. The specific tissues collected were fetal whole ovary; neonatal whole ovary; prepubutal whole ovary; 2, 4, 6 and 8 mm growing follicles; Day 0 follicles; Day 5 small antral follicles and corpora lutea; Day 12 corpora lutea and Day 12
/collicles. More information regarding the methods can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://genome.rnet.missouri.edu/Swine/Methods.html.
Library Construction (Standard Protocol): All procedures
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elsewhere (Soares et al., 1994; Bonaldo et al., 1996;
Jiang et al., 2001). Total cellular RNA from each sample
was isolated by using STAT-60 reagent (Tel-Test,
Friendswood, TX) and the poly(A)+ RNA was obtained by two
rounds of purification with the Oligotex mRNA isolation
kit (Qiagen) according to the manufacturer's instructions provided with the
SuperScript Plasmid System (Invitrogen, cat. no.
18240-013). Britefly, 1mg of poly(A)+ RNA will be annealed
at 37 degrees Celsius with 10mg of NotI-tag-dil8
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xref="taxon:9823"
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/dev_fatge="Perinatal ovary"
/clone lib="pnatal"
/clone lib="pnatal"
/note="Vector: psport; Funding: A grant from the Monsanto Company to the University of Missouri. Genetic Source: Ovarian tissue (whole ovary, dissected follicles, or corpora lutea) was collected from crossbred pigs (Sus scrofa domestica), frozen in liquid nitrogen shortly after collection, and stored at -80 degrees Celsius until RNA extraction. The tissue from several individual pigs was pooled for the purpose of RNA extraction. The specific tissues collected were fetal whole ovary; neonatal whole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jiang H., Whitworth, K.M., Bivens, N.J., Ries, J.E., Woods, R.J., Forrester, L.J., Springer, G.K., Mathialagan, N., Agca, C., Prather, R.S. and Lucy, M.C.
Large-scale Generation and Analysis of Expressed Sequence Tags from
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Library Construction (Standard Protocol): All procedures
discussed in this section have been described in detail
elsewhere (Soares et al., 1994; Bonaldo et al., 1966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus
2. Jiang H, Bivens NJ, Ries JE, Whitworth KM, Green JA, Forrester LJ, Springer GK, Didion BA, Mathialagan N, Prather RS, Lucy MC (2001) Constructing cDNA libraries with fewer clones that contain long poly(dA) tails. Biotechniques 31:38-42. 3. Soares MB, MF Banaldo, P Jelene, L Su, L Lawton, A Efstrantiadis. 1994. Construction and characterization of a normalized CDNA library. Proc Natl Acad Sci. 91:9228-9232.
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Contact: DNA Core Facility (Swine Project)
Animal Science - RS Prather
University of Missouri-Columbia
MG16 Medical Sciences Bldg., Columbia, MO 65212, USA
Fat: (573) 882-6428
Fax: (573) 884-5552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
                                                                                                                                                                                                                                library, Proc Natl Acad Sci, 5
TAG TISSUE-8mm ovarian follicle
TAG_SEQ-Not found"
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/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
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JOURNAL

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ORGANISM

REFERENCE AUTHORS

ACCESSION VERSION KEYWORDS SOURCE

RESULT 8 CO954011

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Sequence localization (http://genome.uiowa.edu/pubsoft/software.html) present in the oligomucleotide used to prime first-strand synthesis. Second strand synthesis was performed with T4 DNA polymerase in the presence of DNA ligase and RNase H. After second strand synthesis, the double-stranded CDNAs was ligated to SalI adapters (Invitrogen-Life Echnologies). The CDNAs wail) be size selected by passage through CDNA size fractionation columns (Invitrogen-Life technologies). The CDNAs wail be size selected by passage through CDNA size fractionation columns (Invitrogen-Life technologies). The CDNAs will be size selected by passage through cDNA size fractionation columns (Invitrogen-Life technologies). The CDNAs will be size selected by passage through cDNA size fractionally into the NotI and SalI sites of the pSPORTI vector

(Invitrogen). After ligation of the inserts, the plasmids will be electroporated into DH10B bacteria. Preliminary Library were analyzed by restriction digestion to determine average insert size (96 clones) and by sequencing (~4 96-well plates) to confirm library quality [e.g. the presence of short poly4+ tails, genomic DNA contamination (must be <1%), ribosomal RNA clones (must be <1%) etc.] and to provide a sequence database representing the predominant clones in each library. The clones were sequenced at the University of Missouri-Columbia DNA Core Facility. Bioinformatics group (WG Spollen, JR Ries, A Guillen, AA Khambati, RV Patel, CM Topinka, SB Bhuiyan) in Computer Science and Health Management and Informatics Departments at the University of Missouri-Columbia. Clone Requests: Requests for clones should be made to the Director of the University of Missouri-Columbia. Clone Requests: Requests for clones should be made to the Director of the University of Missouri-Columbia. Clones Requests: Requests for clones with fewers. Boringer GK, Didion BA, Mathialagan N, Ries JB, Whittworth KM, Green JA, Forrester LJ, Springer GK, Didion BA, Mathialagan N, Ries Park Missouri DNA CORE dacillate and Park
Jiang et al., 2001). Total cellular RNA from each sample was isolated by using STAT-60 reagent (Tel-Test, Friendswood, TX) and the poly(A)+ RNA was obtained by two rounds of purification with the Oligotex mRNA isolation kit (Qiagen) according to the manufactures' sinstructions. The libraries were constructed essentially as described by the manufacturer's instructions provided with the SuperScript Plasmid System (Invitrogen, cat. no. 18148-013). Briefly, Img of poly(A)+ RNA will be annealed at 37 degrees Calsius with 10mg of NorI-tag-dT18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transcribed at 37 degrees Celsius with SuperScript II (Invitrogen) reverse transcriptase (diang et al., 2001). The 'tag' represents a tissue/stage-specific ten-base sequence identifier
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Jelene, L Su, L Lawton, A Efstrantiadis. 1994.
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EST 21-JUL-2000

linear

mRNA

451 bp

BE403103

RESULT 9 BE403103 LOCUS

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Submitted (01-OCT-2001) BBMI, Institut Pasteur, 25, rue du Dr
                                                                                                                Pasteur.
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                                                                                                     Triticum aestivum (bread wheat)

Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooideae; Triticeae; Triticum.

E 1 (bases 1 to 451)

S Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T.,

Cloutier,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A.,

Gustaffson,P., Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J.,

Joudrier,P., Langridge,P., Lazo,G.R., Lin,J.J. McGuire,P.,

Shariflou,M., Sorrells,M., Warburton,M. and Wenzel,G.

International Triticeae EST Cooperative (ITEC): Production of

Expressed Sequence Tags for Species of the Triticeae

L Unpublished (2000)

Contact: Jacquemin JM

Centre de Recherches Agronomiques, Departement de Biotechnologie

234 chaussee de Charleroi, 5030 Gembloux BELGIUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNS07H85 455 bp DNA linear GSS 02-OCT-2001
Anopheles gambiae GSS T7 end of clone 25H23 of library NotreDamel
from strain PEST of Anopheles gambiae (African malaria mosquito),
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Submitted (01-OCT-2001) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
    GBX Wheat Root Library Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/cultivar="Odeon"
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Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3mail: jacquemin@cragx.fgov.be
International Triticeae EST Cooperative (ITEC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - Web : www.genoscope.cns.fr)
2 (bases I to 455)
Roth, C. W., Brey, P.T., Ke, Z. and Collins, F.H.
Direct Submission
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Anopheles gambiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Triticum aestivum"
                         cDNA clone GBX002.C11, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://wheat.pw.usda.gov/genome_
Location/Qualifiers
  GBX002.C11F990602#08 ITEC
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                                                                     BE403103.1 GI:9362483
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Fax: 32 81 61 04 59
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/tissue_type="Whole Plant"
/clone_lib="Arabidopsis_RT-PCR Products (CSHL)"
/clone_lib="Arabidopsis_RT-PCR Products (CSHL)"
/note="DNA wase sextracted from Arabidopsis thaliana whole plant tissue, provided by members of Rob Martienssen's lab, using TRIZOL. Primers were designed in Hypothetical genes and un-annotated regions in Arabidopsis that are conserved in Brassica oleracea located in the short arm of chromosome 4. PCR products were either cloned into pCR chromosome 4. PCR products were either cloned into pCR TOPO 2.1 vector (Invitrogen) and then sequenced using -21 M13 forward and reverse universal primers or treated with Exonuclease 1 and Shrimp Alkaline phosphatase and sequenced using the specific primers."
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
Roux, Paris 75015, France
This clone is from an A. gambiae BAC library provided by F.H.
Collins and sequenced by Genoscope in collaboration with the
Laboratory of Biochem. and Biol. Molec. of Insects, Institut
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500 Sunnyside Blvd., Plainview, NY 11797, USA
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Katari,M.S., Balija,V. and McCombie,W.R. Arabidopsis RT-PCR Products (CSHL)

Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36.8; DB 9
Pred. No. 0.001;
0; Mismatches
                                                                                                                                                                                                   gambiae"
                                                                                                                                                                                                                                                                                   /db_xref="taxon:7165"
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/note="end : T7"
                                                                                                                                                                                                                                    /mol_type="genomic DNA"
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High quality sequence stop: 591.
Location/Qualifiers

    .455
    /organism="Anopheles

                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 516 422 4086
Fax: 516 422 4109
Email: mccombie@cshl.org
matches At4g04920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.6%;
Similarity 85.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41; Conservative
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Pujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Direct Submission
and Chemical Research (RIKBN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(B-mail:chimpbes@gsc.riken.go.jp, URL.http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of primers
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Pan troglodytes DNA, clone: PTB-135016.F, genomic survey sequence.
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Buharyota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammālia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
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Direct Submission
    Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
                                              Taylor, T.D., Yada, T.,
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/clone_lib="PTB Chimpanzee Male BAC Library"
                                              Fujiyama, A., Hattori, M., Toyoda, A.,
Tockti, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
Unpublished
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-041G18.F"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequencing: -21M13
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R.Site 1 : SacI
R.Site 2 : SacI
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AUTHORS
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AG125607
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Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission

Birect Submission

Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gec.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
TT-1:81-81-45-503-9111, Fax:81-45-503-9170,
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
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Pan troglodytes DNA, clone: PTB-059B24.F, genomic survey sequence.
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Pan troglodytes DNA, clone: PTB-041G18.F, genomic survey sequence.
AG055437
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
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Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                   Gaps
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Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end seguences of Library PTB
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/ Match 73.6%; Score 36.8; DB 7; Length 591; Local Similarity 85.4%; Pred. No. 0.0011; les 41; Conservative 0; Mismatches 7; Indels (
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Pred. No. 0.0011;
0; Mismatches 7; Indels (
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/clone_lib="PTB Chimpanzee Male BAC Library"
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-059824.F"
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Best Local Similarity 85.4%;
Matches 41; Conservative (
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R.Site 1
R.Site 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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VERSION
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KEYWORDS
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COMMENT

LOCUS

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Gaps

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Submitted (02-MUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gcr.riken.go.jp, Wil:http://hgp.gsc.riken.go.jp/, T=1:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
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Pan troglodytes DNA, clone: PTB-127D11.F, genomic survey sequence.
AG118925
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Pan.
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Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
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                                                                                                                                                                                                                             sex="male"
'cell_type="lymphoblast"
'clone_lib="PTB Chimpanzee Male BAC Library"
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/clone_lib="PTB Chimpanzee Male BAC Library"
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                                                                                                                                          /organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-135016.F"
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/db_xref="taxon:9598"
/clone="PTB-127D11.F"
                                                                                                   Location/Qualifiers
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Pan troglodytes
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                                       : pKS145
: SacI
: SacI.
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R.Site 1 : SacI
R.Site 2 : SacI.
Sequencing: -21M13
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                                         Vector
R.Site 1
R.Site 2
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Best Local Similarity
Matches 41; Conserva
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KEYWORDS
SOURCE
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73.6%; Score 36.8; DB 9; Length 682; 85.4%; Pred. No. 0.0011; ive 0; Mismatches 7; Indels

41; Conservative

Query Match Best Local Similarity Matches 41; Conserv

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3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 50
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Search completed: May 10, 2005, 07:25:15 Job time : 353.316 secs

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Drosophi

Kanthomo Drosophi Human DNA 1 15 Homo sap:

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Run on:

Sequence:

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unclassified.

I (bases 1 to 564)

S Grigliatti.T.A., Theilmann, D.A., Pfeifer, T.A. and Hegedus, D.D.

Insect expression vectors
Insect expression vectors

A patent: JP 2001516225-A 1 25-SEP-2001,
THE UNIVERSITY OF BRITISH COLUMBIA

ON Multicapsid nucleopolyhedrovirus

PN JP 2001516225-A/1

PP 25-SEP-2001

PR 27-MAR-1999 US 60/049946, 28-JAN-1998 CA 2221819 PI

THOMAS A GRIGLIATTI, DAVE A THEILMANN, THOMAS

A PFEIFER, DAVENE D

PI HEGEDUS

PC C12N15/85, C12N5/06, C12N15/69/C12N9/22

CC Insect expression vectors

FT source Location/Qualifiers

FT Source Location/Qualifiers
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AX766573 Sequence
M83827 Orgyia pseu
U75930 Orgyia pseu
AF512031 Choriston
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A121979 Mus muscu
CR381569 Danio rer
AP003376 Oryza sat
AC134482 Rattus no
AC13555 Rattus no
AP005031 Streptomy
BD221352 Human gen
AY327402 Choriston
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7998.346 Million cell updates/sec
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           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                    US-09-896-888A-1_COPY_351_527
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Maximum Match 100%
Listing first 45 summaries
                                                              nucleic search, using sw model
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Database

PAT 27-AUG-2002

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Homo sapi Human DNA

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Continuation (3 of AL939130 Streptomy CQ597684 Sequence CQ610737 Sequence

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CQ597684 CQ610737

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NPHTTAA 1100 DNA linear VRL 02-AUG-1993 Orgyia pseudotsugata nuclear polyhedrosis virus transcriptional trans-activator (IE-2) gene, complete cds; ORF, complete cds.
                                                                                                                                                           Klysner,S., Nielsen,P.S., Bratt,T., Voldborg,B. and Mouritsen,S. Novel immunogenic mimetics of multimer proteins patent: WO 0304244-A 60 22-MAY-2003; Pharmexa A/S (DK); Klysner, Steen (DK); Nielsen, Finn Stausholm (DK); Bratt, Tomas (DK); Voldborg, Bjorn (DK); Mouritsen, Soren
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Best Local Similarity 100.0%; Pred. No. 5.9e-41;
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2551. .2556
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/note="EcoRI site"
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/note="Aval site"
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/note="ClaI site"
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/note="ClaI site"
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Location/Qualifiers
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                                                                                                                                            1 GTCTTATCGTGACAGGACGCCAGCTTCCTGTGTTACTAACCGCAGCCGGACGCAACTCCT
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100.0%; Score 177; DB 14; Length 1429;
Best Local Similarity 100.0%; Pred. No. 6e-41;
Matches 177; Conservative 0; Mismatches 0; Indels 0;
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/gene="p8.9"
/note="8.9 kda basic protein"
/codon_start=1
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Seguence 60 from Patent WO03042244.
AX766573
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NYNSNFVTSTECNHAVCFKCYVSIVEGKESYKCSICNRTTISCRAYNEDGYVELSTRNS
TVRDSQAIKRHWAQLSDSNMPHSNBMTTIQELQAELAELRAATARAHHDVNWARSDSQ
LLRQQLDVKGAELAHESNARLKLQKQNFTLSANNLSLQHQLNTQVIESRVKWEGFKRQ
HDEFMEKFKLSLS."
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3954. .3559
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Roraynlheavnrherlrrelgermtrsptyllnyspsysptsprsrspdlimpedlop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="ORF; homologous to the ACMNPV PE-38 gene; putative"
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PNSVVSCKFIKKTGDRTPACLQPMLALKTIQDRYMATEEEBATEPSFVIKNLQAQLDA
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                                                                                                                 2 (bases 1 to 4170)
Theilmann, D. A. and Stewart, S.
Tandemly repeated sequence at the 3' end of the IB-2 gene of the Baculovirus Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus is an enhancer element
Virology 187 (1), 97-106 (1992)
                                                                                                                                                                                                                                                                          Original source text: Orgyia pseudotsugata nuclear polyhedrosis virus DNA.
1 (bases 1 to 4170)
Theilmann, D.A. and Stewart, S.
Molecular analysis of the trans-activating IB-2 gene of Orgyia
pseudotsugata multicapsid nuclear polyhedrosis virus
Virology 187 (1), 84-96 (1992)
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protein id="AAA46749.1"
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627. .3959
                                                                                                                                                                                                                                                                                                                                                                   nuclopolyhedrovirus"
                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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2984
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627. .634
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657. .>1908
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2915. .2922
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2944. .>3907
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/noce="similar to Autographa californica nuclear
polyhedrosis virus (AcMNPV) deposited in GenBank Accession
Number L22858"
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KATAAHSPSADEINVHDLMSDHPSFVDMYFCYSBPTAMAIVMDYVPCPDLFFTLQTO
GALDNALVVNI VRQLCDALMDLHNATSYINDVCKLENVLYFGARDRYXLCDYGLCKRE
HSPVHDGTLEYFSPERTRENRYARSPDWYAVCVLAYKLLTGGRHPFERSADBYLDLAS
MRRRQQYNDPAALKNVRNLMARDFVFCLTRFNFECRSTDYKQIAKHSFLASRHDYI"
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Orgyia pseudotsugata multicapsid nucleopolyhedrovirus, complete
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Ahrens, C.H., Russell, R.L., Funk, C.J., Evans, J.T., Harwood, S.H. and Rohrmann, G.F.
The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear polyhedrosis virus genome
97271309
                          540 TATCGGAACAGGACGCGCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACA 599
                                                                                                                                                         600 CGAGGCGCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAAA 656
                                                                                                                        121 CGAGGCGCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 177
61 TATCGGAACAGGACGCCCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACA
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On Oct 26, 2000 this sequence version replaced gi:2934903.
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nucleopolyhedrovirus"
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/note="ORP1; pk-1; similar to AcMNPV ORP10"
/codon_start=1
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/note="ORF2; similar to AcMNPV ORF9"
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/product="1629-capsid"
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COMPLEMENT (8180...9142)
/note="ORF12; similar to AcMNPV ORF13"
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/LTAILS OITELATED.
/LTAILS OITELATED.
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COMPLEMENT (9094. 9825)
/note="ORF13; lef-1; similar to AcMNPV ORF14"
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PLERRLNESVDGAVYVSFGSGIDTNSIHAEFLQMLLDTFANLNNYTVLMKVDDAVAAS
VALPRNVLAQKWFSQTAVLRHKNVVAFVTQAGLQSSDBALQARVPMVCLPMMGDQFHH
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                                                                                                                                                                                                                                                                             /translation="MLTSRRWAVIYTRTSERNCGGAWCTNGYRRRQVHLPSYRARAM
PPDRWHEYTACGAVIEGTRLLCFKVPLNAELFEYVTSDEDRWTAASVLARHSALGAVI
DLINTARYYDGAQMYKMGLLYKKIRVPGRAVPDDDIVAEFIETVDEFFRRCPTWLVAV
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TADNYMGLI EMFKDQFDNANVRRFLSTNRTFDAVVVBAFADYALVFGHLFRPAPVI QI
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PIRHALGLPVGDHIHVYCEAAPTCAALPNAMPALYDYMVRRIGEGKRVLVHCYAGASR
SAALAVYYLMRSRQMPYQDALNAVQSKRRVAINDHFVRFLATRCSYRFVNDELKPQIV
                                                                                                                                                                                                                                                                                                                                                                           HWTHGLNRSGYLVCRYMVERLGVSPTDAIARFETARGHKIERTNYLQDLLARKHVRGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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/product="ecdysteroid UDP-glucosyltransferase"
                                                                                                                              ORF1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9893. .11362
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                                                                                                                           note="ORF10; ptp-1; similar to AcMNPV ORF
/codon_start=1
product="protein tyrosine phosphatase 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                            6819. .7814
/note="ORF11; similar to AcMNPV ORF11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similar to AcMNPV ORF16"
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; Pred. No. 5.2e-41;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="unknown"
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/db_xref="GI:1911260"
                                                                                                                                                                                                                      /protein_id="AAC59009.1"
/db_xref="G1:1911256"
                                                                                                 .6791)
                                                                                                    complement (6129.
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/note="ORF15; si
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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Best Local Similarity 100.0
Matches 177; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Н
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="late expression factor 2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RRFGFLSRNVLVSACMAVNVQVYAPDATĪDMRHQPTIYFRVCQNCHAMADVPAPDDHS
IARYLLAECGAVLVIDHPLDVFGETEEGVNELLEVQRINAGGDL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'translation="MNRPTMRNTAAVTTDYDREQLRRELNSLRRSVHELCTRSATGFD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MYEASQIDEHVFVGGYYGDNEAMLRFIENHAIASVISLIDSDVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="wgasgnsegktiklfyrmssgtgaalddekdlhclydlerfyga
hinkraddkarkkkcaekaalkryelaadrhmleaaaapacaddgrmstlsraqlddi
arekelydrihrlolkqdsllkqdrlkkr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MPGARFVRFSLRLTQEFKENVVAHVDHLMGLRALIDGKVTSADV"
                                                                                                                                 RNLNSVLÄR I BALLRVDVVNDAEVNVLSGDFYEEYSKYI SYQQTFAQTPTASASQOTQ
TSLPRPQTSLPRQTQASLPQQTPFDQPEMVSPPSFVHTTPAI LPQTTQPPATDTFSRP
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                                                                                                                                                                                                                               VTTSMPPPPPPPSADVTTSMPPPPPMVDLATSMPPPPPPPPPMVDLATSMPPPINNA
                                                                                                                                                                                                                                                                INNLLIDAMVAETNKNAGDNRSALLDQIKQGKTLKKTQPADGAPATDPRSTLLSEIRQ
                                                                                                                                                                                                                                                                                          GKTLKKLRKI EDQSSTQTLLKDVDTTDKTKTILKNFVTNIDRISKQEQEEKDRLDTIT
KRRPAVEHTDGNSTGNNSDDWRDD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MRKNNGASQYPEHLTTVHKRHRLQLSCVWCDDQRSWDPHSAKGL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(4125. .4739)
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                                                                                                                                                                                                                                                                                                                                                       complement(2533. .3270)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5020. .5460
/note="ORF8; similar to AcMNPV ORF4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(4742. .4975)
/note="ORF7; similar to AcMNPV ORF5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CNRFLEAGDRAPAVIVKAAANGGQHSSLICDKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EILIEVSLVFKVKEFAPDAPLFTGPAY"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein id="AAC59003.1"
db xref="GI:1911250"
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db_xref="GI:1911251"
            id="AAC59001.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MFEHMFCCLRIYVQQKIKH"
complement (3698. .4093)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (3350. .3541)
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product="unknown"
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fumiferana multicapsid nucleopolyhedrovirus genomic region encoding the regulatory genes pkip, p47, lef-12, and gta Virology 271 (1), 109-121 (2000) 20276145 10814576 6 8 (bases 1 to 129609)	Carstens, B.B., Liu, J.J. and Dominy, C. Identification and molecular characterization of the baculovirus CfMNPV early genes: ie-1, ie-2 and pe38 Virus Res. 83 (1-2), 13-30 (2002) 21854555 11864738		de Jong, J.G., Dominy, C.N., Lauzon, H.A., Arif, B.M., Carstens, E.B. and Krell, P.J. Direct Submission Submitted (13-MAY-2002) Department of Microbiology, University of Guelph, Chemistry and Microbiology Building, Guelph, ON NIG 2W1,	Canada I to 129609) de Jong, J.G., Dominy, C.N., Lauzon, H.A., Arif, B.M., Carstens, E.B. and Krell, P.J. Direct Submission Submitted (13-MAY-2004) Department of Microbiology, University of Guelph, Chemistry and Microbiology Building, Guelph, ON NIG 2W1,	Canada Sequence update by submitter On May 13, 2004 this sequence versi Location/Qualifiers 1129609 /organism="Choristoneura f	/db_xref="taxon:208973" /country="Ireland" country="Ireland" complement (I735) /note="0RF1; Ac8/Op3" /codon_start=1 /product="polyhedrin" /protoctin_id="AAP29795.1"	/trānslation="MPDYSYRPTIGRTYVYDNKYYKNLGSVIKRKRKHLLEHEEDEK HLDPLDHYWARDPELGPGKOKGYLTPKETRNWKDTNKLIYWNSGKEEDEFFWTRFV EDSPPTWIDGWWDVELVYWNRPTRENRCYKETRGHALRWDCDYVPHEYIKTIYEFW GRNNEYRISLAKKGGGCPIMNIHAEYTNSFESFVNRVIWENFYKPIVYIGTDSGEEEE MLIEVELVFKYKKRERADDAPLFTGPAY" Complement (838 . 1449) /note="ORF2; Ops" /codom state:=1	196.1" 880" VEDRRAAALLQDGCQ LOLLVGYSKHGKNAA RCDAKAKKNKCAEKA RCDAKAKKNKCAEKA DIVDRIYQLQLKQDR 1859) Ace(Ope"	/product="late expression factor 2" /protein_id="AaP29797.1" /db_xref="d="AaP2997.1" /db_xref="d="id="AaP29981" /translation="MDQVWNPAAGAGSVKKPETYLIDPNDFVGMLELTPYTVFERGLF IRMSGMELLALLAAPKRVPTTRRFPGRSKRNVCLKECADGPGSLTKVLTARNMMPLC MSKIMADLGSAPRGNMYRKRFFFNCYLANVLTCTKCKAACLIGALLHFYRMDAKCVGE VTHLLIKAENTYKPSNGAKKAVTKLCPKANNCKGLNPICNY" complement(18622092) /note="ORF4; Ac5/Op7"
JOURNAL MEDLINE PUBMED REFERENCE	AUTHORS TITLE JOURNAL MEDLINE PUBMED	REFERENCE AUTHORS TITLE JOURNAL REFERENCE	AUTHORS TITLE JOURNAL	REFERENCE AUTHORS TITLE JOURNAL	REMARK COMMENT PEATURES SOURCE	CDS	CDS	CDS	CDS
	121 CGAGGCGCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 177 	c AF512031 N Choristoneura fumiferana MNPV polyhedrin, complete genome. R AF512031 AF17329 S78506 S81690 U10441 U18677 U26676 U26734 U53854 M57401 U59008 U70432 U72240 X65395 S46001 AF512031.2 GI:47157118	Σ	Lee Ide Cho Vir 930	<pre>2 (Dases 1 to 129609) Xie,W.D., Arif,B., Dobos,P. and Krell,P.J. Xie,W.D., Arif,B., Dobos,P. and Krell,P.J. Identification and analysis of a putative origin of DNA replication in the Choristoneura fumiferana multinucleocapsid nuclear polyhedrosis virus genome Virology 209 (2), 409-419 (1995) 95297142.</pre>		4 (Bases 1 to 129609) 4 (Bases 1 to 129609)  Barrett,J.W., Krell,P.J. and Arif,B.M. Characterization, sequencing and phylogeny of the ecdysteroid UDP-91ucosyltransferase gene from two distinct nuclear polyhedrosis viruses isolated from Choristonara fumiferana J. Gen. Virol. 76 (Pt 10), 2447-2456 (1995) 7595348	5 (bases 1 to 129609)  Qiu,W., Liu,J.J. and Carstens, E.B. Studies of Choristoneura fumiferana nuclear polyhedrosis virus expression in insect cells Virology 217 (2), 564-572 (1996) 96183379 8610448 6 (bases 1 to 129609) Liu,J.J. and Carstens, E.B.	Identification, molecular cloning, and transcription analysis of the Choristoneura fumiferana nuclear polyhedrosis virus spindle-like protein gene Virology 223 (2), 396-400 (1996) 96400202 8806578 7 (bases 1 to 129609) Lapointe,R., Back,D.W., Ding,Q. and Carstens,E.B. Identification and molecular characterization of the Choristoneura
Db 128! Qy 128!		KESULI 6 AFS12031/C LOCUS DEFINITION ACCESSION	KEYWORDS SOURCE ORGANISM PREFERNICE	AUTHORS TITLE JOURNAL MEDLINE PUBMED	REFERENCE AUTHORS TITLE JOURNAL MEDLINE	PUBMED REFERENCE AUTHORS TITLE JOURNAL MEDLINE	PUBMED REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED	REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE

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Pseudomonas putida KT2440

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

Beadomonadacea; Pseudomonas;

CE 1 (bases 1 to 300363)

RN elson, K., Paulsen, I., Weinel, C., Dodson, R., Hilbert, H., Fouts, D., Gill, S., Pop, M., Martins Dos Santos, V., Holmes, M., Brinkac, L.,

Beanan, M., DeBoy, R., Daugherty, S., Kolonay, J., Madupu, R.,

Rizzo, M., Lee, K., Kosack, D., Woestl, D., Wedler, H., Lauber, J.,

Hoheisel, J., Straetz, M., Heim, S., Kiewitz, C., Bisen, J., Timmis, K.,

Duesterhoft, A., Tummler, B. and Traser, C.

Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440

AL Environ Microbiol. 4 (12), 799-808 (2002)

CE 2 (bases 1 to 300363)

CE 2 (bases 1 to 300363)

Rolson, W., Martins Dos Santos, V., Holmes, M., Brinkac, L.,

Beanan, M., DeBoy, R., Daugherty, S., Kolonay, J., Madupu, R.,

Holtzapple, E., Scanlan, D., Tran, K., Moazzez, A., Utterback, T.,

Rizzo, M., Lee, K., Kosack, D., Moestl, D., Wedler, H., Lauber, J.,

Rizzo, M., Lee, K., Kosack, D., Moestl, D., Wedler, H., Lauber, T.,

Rizzo, M., Lee, K., Kosack, D., Moestl, D., Wedler, H., Lauber, J.,

Rizzo, M., Lee, K., Kosack, D., Moestl, C., Eisen, J., Timmis, K.,

Duesterhoft, A., Tummler, B. and Fraser, C.

Direct Submited (05-NOV-2002) The Institute for Genomic Research, 9712

Medical Center Dr., Rockville, MD 20850, USA

Location/Qualifiers
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PPAPLLAAPRIPGALDADDDETYRAGLLVEVDPYPELELGDSLVLYAVGFEVTLR
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GHGSTGAAI UPRPPSGDTRLFTVPRSAMAANIGRILMYYYTVTRAGETERRISEKTELR
VSDPORSYPITQVEGAENBELKLHSVPGALCTLPPWTFWABGQLIGIEAGRSAS
GQDVTHILRPPTEAVTYDEYSDGVIKAYLPKQFIGNILDIGKDFRITVSASFDDGETWR
                                                                                                                                                                                                                 BCT 12-DEC-2002
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                                                                                                                                                                                                              AB016781 300363 bp DNA linear BCT 12-DEC-20
Pseudomonas putida KT2440 section 8 of 21 of the complete genome.
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/note="identified by Glimmer2; putative"
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1. .300363
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| mol_type="genomic DNA"
| fstrain="KT2440"
| db_xref="taxon:160488"
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78. .1985
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2024. .4489
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JOURNAL
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AUTHORS
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SOURCE
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                                                                                                                                                           RESULT 7
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SAALVVYYYMRSRQMSYEEALSLVKNKRRVAISNHFVRFLASKCSYKFVNNVLKIRVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="protein tyrosine phosphatase 1"
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/translation="wFDRWHFFPCGRVIDGTRLICFKVPLSAELFBYVTNDEDRWT
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VDEFQDRCFTMLVGVHCTHGLNRSGYLVCRYWVDKLGVSPADAIIRFEERARGHKIERA
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db_xref="GI:30269988"
'translation="MHSVRNLFDSNMSLSSKLLVYAYYGAFNLLHEKYGESYHLYRIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HEHLTETYVSNASCVRRDIATARCFENGFCFNLARQLLDVTDVAARLAAWYNRGDKTG
LCANVQLALAEIDKYAPLEKRVSIGNNIFALDTIADIPSNALDDFQTIIYBGFKDFVD
MNNLAHVADVFDFDPKIKAEGWWYYKPCVLTYMHRLTVNAVFTELWTRLQDAVIKFVQ
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/translat_ion="MPNFVKFSLRITRESKENIVAHIGHLSRVRELIDRNVTPADVRR
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db_xref="G1:30269985"
'translation="WAMLKTFLLICVSSAALSVKVTTINNVLYTVNDTQKTIAVKQVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DKPAFIQVIPPQSFTKNQEELDMLHHPPGVASNVMFPRIANNTKLTVLLSDGSLATIT
VDRVTVHPHSHKNRMYYGQVSFALLSNSSLAMQIYIGAPIPEKERMVSVITARHEDYK
NKLVIYPPTGISAEGLYSGQINFDLQILTQKLLEGSSVYGKNQLPYKALKDYAISTNR
NKNLFKGLPRNVAVFYNERDITIALVEGFFEIDRIRLSGPLILRNIKQQ"
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KDFGRLCKETYTDLRAEADLLYINATTDEKKNALFDLLCCVNAADLDVDCYDYIVDNF
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CNRFLDGVDKAPAVIIKPAAAGQHSSLICDKV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MDRNIKKNAVTDTWIFKMCIHYTRTGIHHPCLSNSFVKRPVYLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'product="protein tyrosine phosphatase 2"
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product=-baculovirus repeated ORF"
protein_id="AAP29800.1"
db_xref="GI:30269984"
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/note="ORF9; ptp1; Ac1/Op10"
/codon_start=1
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                                                               protein_id="AAP29798.1"
db_xref="GI:30269982"
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/note="ORF8; ptp2; Op9"
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                                                                                                                                                                                        2137. .2568
/note="ORF5; Ac4/Op8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHTVLINNNYAQDAPQFAI"
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/note="ORF6;Ac2"
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Best Local Similarity
Matches 37; Conserv
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LSESDINVOSEI ILPTANQARWRFTYEDVILGYLCVRECTTPYGGGGENEVEYCOAGHKEPS.
SAARDKULENTREIDPREGQAAKVVRYEYPGTHMETGGGSSISWSDOCLDINLYKUP
EDYTYKSI OI OEVRAGSVATITRENR FILLTEQATAQGDKILQAFTRYADNAGNFES
OEPF FQLPHDETQRWSLISPRENGRERKAVTRYDSHGNVLTRILDNQVLETNVWYSAE
ERGDEHGFVRNLKTRYOPAATGHGAAATTOAFQYRALTPLGSYLKOPWRLLISSETL
SESGSAPGTFLEKI SKLYOBESARFS SYGRVRQOTVSYPGVDGGSPFDTLTHYGYSLP
DBERALQTVEKLVOYDGESKTI TLAHALDTGEPLINLDDNGVBI RYYYDALRRYTREV
VAPGKFERARNYKYFLCAYDNEGAQWAYDVRQVYSTHTLLDGLSRP I FEBRADNGSA
TYAGALRP I YRARYDELDQLVEETEI DMLGGGGLLELTSHI SYDDWGGRYAVLNPDGTT
QVBEI DQVASTDGPPHRANREVHERVSGTTETWYNLFEKPANERVRHYNL
RYDDGLGRLSREAAGGGGAGGRYVBYRYDAPDRYNLFEKPANERSHPLISN
PVSI KVGNTESAANTLLGGOVFDGLERRYATHTGGREGOFFWARAPDGTR
I BYQYRPALGEBPYLLAKABOTTATGREGOFFE DDEGROPHWARAPDGTR
I SYQYRPALGEBPYLLAKABOTTATGREGOFFE DDEGROPHWARAPGTR
I SYCYRPALGEBPYLLAKABOTTATGREGOFFE DDEGROPHWARAPGTR
I SYCYRPALGEBPYLLAKABOTTATGREGOFFE DDEGROPHWARAPGTR
I SYCYRPALGEBPYLLAKABOTTATGREGOTE DDDUGRLEKTTLLARPEP
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MKEQKLRQFDLYEDPPGPGGAARFRVEHRSGLVEVLEVMGSGEGEVALPVELHSPLGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RLHLSYLPFGQGHMRLSEVQDESDVLLRLQRSDNSRVELLCYPSGGDDGGPLARYAMT
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RTFDFGDTVQTLAQDYDEFDCLKSRILKERPKGSDESQATLLRHETYQYDRRGRLQIY
TCDGPEAPVDPSGQTIARQIPGFDGLDNILSVITYRPDGSWQRTLYEFKNSDPAQMSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IIPPDALLETYDVDHDLEELFKIVKYDPQLAIDLHYDGNGNLISDEQGRVLTYDGLNR
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LLGPATLATFRHRITLVKTGDLPPGEHQLDGVLVTGHLDWGGFGKVLEYTLRAMVIQT
QCDASADVSANPVDLGEWSVNDFTGPGFTTPPAAFQVRLSNCQVDPDPGNETLATIEL
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FOARFROTEPNSSLRTGLAKGALNFTIRYR"
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                               10329.".14201
/locus tag="PP1887"
/note="identified by match to TIGR protein family HMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                \lambda{ocus_tag="PP1889"
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/locus tag="PP1888"
/note="similar to SP:P42185; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19.7%; Score 34.8; DB 1; Length 300363; 54.8%; Pred. No. 14; ive 0; Mismatches 57; Indels 0;
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/db_xref="G1:24983396"
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/locus_tag="PP1888"
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locus_tag="PP1887"
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/transl_table=11
                                                                                                                                                                                          start=1
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LATVLSKLLEFFTNNEFERPRAENGDLTATA FAGVIAAREKSBYSPYYPYKESYWRGSYD
CLATVLSKLLEFFTNNEFERPRAENGDLTATA FAGVIAAREKSBYSPYYPYKESYWRGSYD
ACVGLWHAEINDELSTYOVIKRRYSORNSMELVTVYHTAADFTRYEET VATPOSWTWGH
ACVGLWHAEINNEITASWQIODLOGATLKLEEYKHKIYPKODGSFRFEGDPYEDOISA
LESFFHVLWAVAAPNVSFYSLSSBRGHAARAALAKDURLDLYMBELINTRIKINFGG
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VEGSSDDPGHPDQHTHGLYLAPGATGIEGEFTRVRVTATVPGGGPASSALLTVVKNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QVSPLLSVCQVGDEGVSLKADSVAEGPLQWRILGASPHGRLAQESGTANRYIPGENLP
DKSPIVEEVEVRNSLTNEHRTLCIVTQMTLKRPSDVVVDKRDEQHARVMLSIHFSEAS
GVDQLTVVHGPGQIDIDEDGKPYYQADAASPAHFCVVGAVWRLSPDLPITLEGFIVLP
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HTFSYBPPREGLTWSLEALPGTYGDLGR I DPASGEYRA PPAHAWAGKPVRVR I I ATDP
STRQAI SAMAVVAPATLITVNPL I RVCYFDDTLTLTAGAQTDLDWSYVDDGEEGRGSV
VAEGDGRRCTYTAGSKYDAVVLDOYRVQNRETSESRS I YTJVNGRRPELVI DVKQ
LPDGDLQLTGMPDGSVGQPDTQWALLPIAGTGEI DBATGRYSPASADADARFALITAKWA
I PGSVFILEGHI I LPLPLSLHFDAARRAAS PTGLRVATS PS I GG"
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APAGARVRADANYGGGALU-YFRLARDSLLAGOGPGTGYPYLLLAPGGYSARTUALWCDML
GHASDDGLELLARLLEPELIARPUKNUSTPLDRVWRGNIDPLATQLTYKFTMGTYVTA
GKTQQPRLYDGKDQLITASAWSVINPQSHDDAGHGSIDGNGLFTAPSPEVIGGEVQTF
ITARYKQGEBFTHAARAALVISEPVAMPARGATRPQGESANGDLMRAGKGNVSFEM
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PPFVPRVGHGETTQLSEVNRIMPNEARRWMLAGPGSVSPSGHPRASELAVSQPNVVT
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SDSRRVRELGGDFFKELFRGLPDHQRVWSFGSIEHGBNDLMRPBEFILERTQRNPGVAL
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QPLLSVTFEHDEVRQHWKSHCTLTFTYKPKPTGPLYSRTATFQFDLQTVFTLNAPASP
EESAGCMLLGQVLWPWQAAEVTEVSGLPSDTPSDLREEIYAFVAFLVKQAVLEGLARE
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LEVTVETMQADGQDYKLCLDEIASIALFDRSGMKIPPLCGDGIDSGSGNVWRTNLKPN
DFIRANESLMATEGQGPQPAAPRGAEDRTIRLQMFLHRRGASTSEVFYAGFQARTGRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MPTNYLSVITTWMKHNHKHLNWDLTPATRPEAINDLLALAHCSQ
PDSALGDIEGETAMPDSDVTHILTGYTRWGPPALVDWQANYTSPKTRGSLEGGSHIV
MDKTDGLLSLSUVHDLLDPLPVTQTVPLSADAQGVSADLREGTDTELDLGGGLPQRQAA
GRFFKEVLSGLGSRAGVYPLADFRALSGNPYLAVRHSSKADGKSALVIPRGI
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NRLLEQQYLTRFKENRYLPPFSHTFAGVGVKEAVSVEALEFGTPLLSFSNASTSDAKA
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DDYMLSYNHGTFYTAEFYKKKESDDNRDVNTENVRMESSFPGBYTKSYTGYVFQXY
EPLPKWYSPDPDSKELLDGVERSSSYYQPGLLAI VNYKRRDLPFNTSDHRALFEKL
SKPLRVQLRDAHANLHI I QIDYLPADTI GDRNI LAHTVOSRPTGRQTSI TRLSNYQER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /locus tag="PP1885"
/note="identified by Glimmer2; putative"
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                       /transl_table=11
/product="hypothetical protein"
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                                                                                                       /protein_id="AAN67503.1"
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6872. .9799
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/transl_table=
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RESULT 8 AC121979 ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

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The RPCI-24 BAC Library has been constructed by Pieter de Jong and coworkers (http://www.chori.org) from male C57BL/67 mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org
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'note="Likely pseudogene (HMM Sc=39.91 / Sec struct
                                                                                                                                                                                                                                                           NEIGHBORING SEQUENCE INFORMATION:
This sequence is the entire insert of the clone.
Location/Qualifiers
1. .155274
                                                                                                                                                                                                                                                                                                                                                                                ı. .1552/4
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="9"
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/clone lib="RPCI-24"
1. .165
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388. .8550
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/rpt_family="Alu"
8319. .8400
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1130_ .1302
/rpt_family="Alu"
4855_ .4982
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5144 . 5254
/rpt_family="Alu"
5316 . 5565
/rpt_family="B4"
5566 . 5711
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77pt family="B2"
788. 936
7rpt_family="B4"
7rpt_family="100"
7rpt_family="MIR"
1104. .1269
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178..287
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/rpt_family="B2"
568. 733
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'670. .7741
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rpt_family="Alu"
876. .4987
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712. .5786
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8826. .9027
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;788. .5975
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http://genome.wustl.edu
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                                                                 SOURCE INFORMATION
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                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (13-NOV-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Nov 2, 2002 this sequence version replaced gi:22476161.
                                                                                                                                                                                                                                                                  AC121979 155274 bp DNA linear ROD 13-NOV-2003
Mus musculus BAC clone RP24-289L14 from chromosome 9, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2001)
3 (bases 1 to 155214)
4 (bases 1 to 155214)
5 (bases 1 to 155214)
6 (bases 1 to 155214)
7 (birect Submission and Waterston, R.H.
7 (bases)
7 (bases)
7 (bases)
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8 (bases)
9 (bases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (25-AUG-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA 5 (bases 1 to 155274) McPherson, J.D. and Waterston, R.H.. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (02-NOV-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
6 (bases 1 to 155274)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 155274)
McLellan,M., Cotton,M., Doebber,A. and Schatzkamer,K.
The sequence of Mus musculus BAC clone RP24-289114
Unpublished (2001)
2 (bases 1 to 155274)
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                                                                                                                                                                                                                                                                                                                                                                         AC121979
AC121979.3 GI:24476151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center code: WUGSC
Web site: http://g
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                                  CGAGGC 126
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                                                                                                                                                                                                                                                                                                                                          segmence.
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note="Likely pseudogene (HMM Sc=33.79 / Sec struct

/rpt\_family="MaLR'

repeat\_region

MAPPING INFORMATION: subspired by Dr. Wes Warren, mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see

restriction digest

repeat\_region

9947. .10098 /rpt\_family="B4" 10110. .10490

Sc=-6.89)

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45478 CCTCACCAGCTCGCACTCTCCTCGGGGGCGCACGGCTCGCCGTGCCCCTGCCCACGG 45537
                                                                                                                                                   CR361569 17-OCT-2004 Danio rerio clone CH211-99120, WORKING DRAFT SEQUENCE, 12 unordered
                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (10-02T-2004) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. B-mail enquiries
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Oct 11, 2004 this sequence version replaced gi:51592229.
                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 179571)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 175712 bases at least Q40
Consensus quality: 175324 bases at least Q30
Consensus quality: 176324 bases at least Q30
Insert size: 178471; sum-of-contigs
Insert size: 179905; 5.5% error; agarose-fp
Quality coverage: 7.91x in Q20 bases; sum-of-contigs Quality
coverage: 8.06x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is
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contig of 45661 bp in length
gap of 100 bp
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of 20408 bp in length
100 bp
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contig of 14830 bp in length
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18311: gap of 100 bp
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contig of 6832 bp in length
gap of 100 bp
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contig of 4450 bp in length
gap of 100 bp
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of 7847 bp in length
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of 9526 bp in length
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of 3824 bp in length
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of 2169 bp in length
                                                                                                                                                                                                                                     DRAFT; HTGS FULLTOP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
------ Project Information
                                                                45538 GACAGAGCGTCCCGCTTCCCTCTCC 45562
                                   123 AGGCGCCCGTCCCGCTTATCGCGCC 147
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gap of
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contig
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HTG; HTGS PHASE1; HTGS I
Danio rerIo (zebrafish)
Danio rerio
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33241:
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114251
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                                                                                                                                                                                                    ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                     CR361569/c
                                                                                                                                                                    DEFINITION
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AUTHORS
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JOURNAL
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/note="Likely pseudogene (HMM Sc=20.93 / Sec struct
Sc=-0.89)"
                                                                  note="Likely pseudogene (HMM Sc=33.19 / Sec struct
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Pred. No. 48;
0; Mismatches 70; Indels 0;
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16036. 16182
/rpt_family="Alu"
16183. 16352
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2093. .12290
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_family="RMER6B"
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7406. .17489
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rpt_family="RMER6B"
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6353. .16501
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/rpt_family="ERVL"
17672. 17818
/rpt_family="Alu"
                                                  product="tRNA-Ser"
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rpt_family="MaLR"
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rpt_family="ERVK"
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rpt family="Alu"
4507. .14582
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/rpt_family="B2"
18962. .19079
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19415. 19480
/rpt_family="B2"
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7585. .17934
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8243. .18309
rpt_family="L2"
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1043. .11114
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family="B2"
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1349. .11370
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1810. .11946
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Best Local Similarity 51.7%;
Matches 75; Conservative
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Sasaki, T., Matsumoto, T., Yamamoto, K., Sakata, K., Baba, T., Katayose, Y., Wu, J., Niimura, Y., Cheng, Z., Nagamura, Y., Azikawa, K., Antonio, B.A., Kanamori, H., Hosokawa, S., Masukawa, M., Azikawa, K., Chiden, Y., Hayashi, M., Okamoto, M., Ando, T., Aoki, H., Azita, K., Hamada, M., Harada, C., Hijishita, S., Honda, M., Ichikawa, Y., Idonuma, A., Iijima, M., Ikeda, M., Ikeno, M., Ito, S., Ito, T., Ito, T., Ito, Y., Ito, Y., Inabuchi, A., Kamiya, K., Karasawa, W., Katagiri, S., Kikuta, A., Kobayashi, T., Muzui, I., Nadahira, K., Machita, K., Machita, T., Mizuno, H., Mizubayashi, T., Mukai, Y., Nakamira, M., Namiki, N., Negishi, M., Ohta, I., Ono, N., Saji, S., Sakai, K., Shibata, M., Shimokawa, T., Shomura, A., Song, J., Takazahi, Y., Terasawa, K., Tsuji, K., Waki, K., Yamagata, H., Yamane, H., Yoshiki, S., Yoshihara, R., Yukawa, K., Zhong, H., Yamane, H., Rodo, T., Ito, H., Hahn, J. H., Kim, H. I., Eun, M. Y., Yano, M., Jiang, J. and Gojobori, T. The genome sequence and structure of rice chromosome 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(1396. 1701,1758. 2043,2410. 2544,
3405. 3547,5098. 5199,6055. 6167,6605. 6690,7352. 7491))
/gene="OSJNBa0014K08.1"
                                                                                Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (join(1396. .1701,1758. .2043,2410. .2544,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Oryza sativa (japonica cultivar-group)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 177263)
Sasaki, T., Matsumoto, T. and Yamamoto, K.
Direct Submission
Submitted (07-MAR-2001) Taknii and taknii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="OSJNBa0014K08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                db_xref="taxon:39947"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chromosome="1'
    clone:OSJNBa0014K08
                                           AP003376.3 GI:21902027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12447438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PUBMED
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene
                                         VERSION
KEYWORDS
                       ACCESSION
                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
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                                                                                    SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACGAGGCGCCCGTCCCGCTTAT 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 AGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGCCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 179571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
154564: contig of 19806 bp in length
154664: gap of 100 bp
179571: contig of 24907 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174954 CCCCCCAAAATCTACAGCATGGAGATTCAGGTTAAA 174919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.5%; Score 32.8; DB 2; Ilarity 50.6%; Pred. No. 54; Conservative 0; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 CGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 177
                                                                                                                                                                                                                                                                                                                              fragment chain:1"
3242." 37691
fragment chain:1"
3242." 37691
fragment chain:1"
37792." 44623
fragment chain:1"
37792." 44623
fragment chain:1"
37792." 59384
fragment chain:1"
fragment chain:1"
fragment chain:1"
fragment chain:1"
fragment chain:1"
09485." 29381
fragment chain:1"
102856." 19381
fragment chain:1"
fragment chain:1"
fragment chain:1"
fragment chain:1"
fragment chain:1"
fragment chain:1"
110256." 110805
fragment chain:1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="assembly_fragment:01746
fragment_chain:1
                                                                                                                                                                                                           1. .18711
/note="assembly fragment:01057
fragment chain:1
clone_end:sp6
                                                                                                          /organism="Danio rerio"
                                                                                                                           /mol_type="genomic DNA"
/db_xref="taxon:7955"
                                                                                                                                                                                       'clone lib="CHORI-211"
                                                                                                                                                                      clone="CH211-99I20"
                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vector_side:right"
                                                                                                                                                                                                                                                                                             rector_side:left"
                                                                                                                                                                                                                                                                                                                   .33141
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Best Local Similarity
Matches 79; Conserval
  134759
154565
154665
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APO03376
LOCUS
DEFINITION
                                                                                          source
                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGIN
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.29650)

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148476 AAGGCCTCGCGCTCTTGTCCGGATTCCGCTGTTGCGCCCCAGCCGCTGAGGCCCCC 148535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="BAC05582.1"
/db_xref="G1:21902033"
/tb_xref="G1:21902033"
/tcmanlat.on="MPVLR8ARRRAREAQENPAAAAAAAAAAPAPPPARRRRAARRKEPEV
AVEAAPEAEGGREEET EVADLGREGGGEKKWEGPDSGARSADKQAYDDGGNTTPVPDT
VQVGSSPKYRVDKKLGKGGFGQVYVGRRMLANGPGASEVALKFEHRTSKGCNHGPPYE
                                                                                                                                                                                                                                                                                                                         AEALRSAAVAFGCFOVVGHGVDRSLVSAALRHVAAATARAATPEPEFVEVNGDDENGE
EMWSPEDGGOGBMAGNWALQSGASHFRNTADALE TOLGEGTATKIMDVLOGRGAVATQS
EAGNDTINGSLLCI FRIRRREQDESFERHDDILRMLYNSSRCSRALALHCPGA
SAFHI FSRRGWSFFRPMDGAVVTVGDQLQACNGGLYKSVAGKPAYSNDDLRGNGGDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35132. 35437)

/gene="OSJNBaO014K08 6"

complement (join(31081. 31242,31391. 31579,31787. 31815,

31903. 31993,32132. 32306,32410. 32549,32638. 32770,

3508. 33574,34086. 34243,34332. 34405,34496. 34609,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WQVYNAIGGIHGVPRVHYKGRQGEYYVIVMTPHFDYYERNCFLFALSKILINLVYEKS
TKWRDASTGLHVDYDQRPDVFREFVEYVNILKFDEEPNYAKCISLPDTVVGPNPDIRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MPYVVGTTGSNCSEALVIRSSLISRQKEEYPKGYGKSELANPPM
AVGPSLDAKSCTFKHICRDYSGERTLCVSVIENRRFAPVSLDVQNKREMVNVLQCLDI
SIFFPC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTDGAÇKLTHLVGÇKRGRLLMBETDEQPKKKTRMGMPATQWISVYNARRPMKQRYHY
YNDSBRLQQHTDKGNBDGLF1SCTTSCSSNLWALLMDAGTGFTSQYYELBPHELMEWN
MDQMERNYYTTALAGANNGSSLVWASKGTWYTQQSYKVVBLDFLYPSBEIHQRWDNGY
RITATAATWDQAAFVLSVPRRKPTDBTQBTLRTSAFPSQHVKKSGHLVBAISSSRLLA
                                                                                                                                                                                                                                                             /trānglation="MATASVVTYLQRPRELPVPEFRAPPPSPVTGVLTSSSSGSLAYG
ECPDSNEDDEIGRFLRRSARVPVLRLPERAVPRKKKAAWAPPVIDVRLLALPEAGGPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                              GVASAELFYCFPSAGTAAGKASEVLSADAGKIIPLNLQFWVAACLVLGYHFLLSSLHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (join(31081. .31242,31391. .31579,31787. .31815,31903. .31993,32132. .32306,32410. .32549,32638. .32770,33508. .33574,34086. .34243,34332. .34405,34496. .34609,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 GTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148416 GTGACAGCGGACGTACGTAATGTGGTTGGAATCTCGCCCCGGTCGAAATTCCTTGGCGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 CAGGACGCCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACACGAGGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="contains ESTs C72949(E2532), C72949(E2532)"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join[39834. .39907,40580. .40722,41299. .41408]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 join(39834. .39907,40580. .40722,41299. .41408)
gene="OSJNBa0014K08.7"
note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 18.3%; Score 32.4; DB 8; Length 177263; 1 Similarity 53.1%; Pred. No. 71; 69; Conservative 0; Mismatches 61; Indela 0.
         .28537,28795. .29152,29378. .29650)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               casein kinase-like protein"
                                                                     .29152,29378.
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join(27978. 28537,28795. 22/
/gene="OSJNBa0014K08.5"
/nocte="hypothetical protein"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /proteIn_id="BAC05583.1"
/db_xref="G1:21902034"
                                                                                                                                                                                                 /proteIn id="BAC05581.1"
/db xref="GI:21902032"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="OSJNBa0014K08.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      product="putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TWLL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 69; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 11
AC134482/c
LOCUS
         gene
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                                                                  CDS
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                                                                                                                                                                                                                                                                                                                         AAIAHLKRCGFYLEKLAKKGRGNSPQRRGGAPRRLRVPTGNEEDDPPPLAPFALPLGR
QWCCCFGPAPPAGAREVRPPRLTWPPRRHPGCPATTPSRHRGLDDPPRHGLAPGGQAE
RRPPPPRFGRPRRAAAIRRLRPPLTNRLYAEPQLSAASAPVPGRPSRSRPPPRRLATG
                                                                                                                                                                                          /translation="MARPDWILERERRQVEQILELDMEELQVEEVDDAGSSSSSEVDT
FLRNTHGDGGSRTSEALAFNTSVVSLPTCDGGVVLFPEAILPIRVVQPRSLTAVDKAV
NHVDAPCMIGVIHHIKQLDDGSSNVVTRGQNRFRLRRRWIDADDVALISRRSDGPVGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /trānslation="MRSMFLPVLPLRACGTGTTAPVPPPTASLRRELALSPNLPARGG
VAGGPNAATREAPAAAVSARRVVVSPSLARRRRTRPPPPPPPLLESPRVEGASPP
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NFVERVYTLFPRDSGRLMSN EQALCRRSFQKVRREHAVLRQKLESYFQLCSCTWAER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MGTVNGEYEDFDAANRRAEVIDWIGGLIPEFDLPLDSSDEELRD
YLINGRALCYVADKLMPGVLEGTWGGYASDQRSNVKKFLSVVAEMGLPGFGVKDLEEG
SMSSIVECLLALKDNVATQLGGHISNSTAKTPIRRKLELRETDGPVLSVATPGKRYPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLDGFNVCI FAYGQTGSGKTYTMSĞPGTSREDWGVNYRALNDLFÖI SLSRKNÄFSYBS
NEAVGSTYALNBRSSRSHSHILTYHWRALDVKNGSPSTSGCHLI-DIDAGSBRYUBRSBATGD
RLKEAQHINKGLSALGDVI FSLAQKNAHVPYRNSKLTQVLQSSLGGQAKTLMFVQIND
DIESYSETI STLKPAERVSGVELQAARSNREGKDI KELLEQVASLKOTI ARKDMEI BQ
SLQLKSKSPNSMTDRNGSNLLARQSTSSTGLSSLPVASQQNQQLSVYTLTPLADTGLAG
SVQLARSKSPNSMTDRNGSNLLARQSTSSTGLSSLPVASQQNQQLSVYTLTPLADTGLAG
SVALARBNASDGCSVGETEYSPAGASETSABRAYLILFSFI SCAKPSCACDTSGE
LMI VPVRLRTGT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QKGILADDRLAKKPSRQYSMEKGSATNRAIPDFRSAAAMSDAMRARRRSPCHARNTR
NGTRRAGARPDPEPSRQPIRVLGGRSLSVDETWVTSPAAAVFLRHGETRAPAFALGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EŠĪĒRKRGEI PHRVYHLLRNVIQEJEHRIGIQADHIRNONSIIKTREDKYRSKIKALE
TLVNGTNEENEMAINRLEVVKVEKSKIDEKRKLGEQDMIRLIREKENAENIIASLHQE
MQVMNRMHEQPRHDLKGLVDAAENYHKVLAENQKLFNEVQELKGNIRVYCRVRPPLPG
                                                                                                                                                                                                                                                                                           YVKQFSCGQEMMTVYNATGLALRGAPSKAHSLFPGPTATPQRRGFEKRCHHGGHDIQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /trānslation="MaITVEWNGQPPSVGHCCIMRPSDVAATCRVQACSCITAAPGGT
GLLREMAGLSSR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SQQRSPLLSGQKINEVVQFKHGTYTDLPAAKISEMLHSNSLDNAPTQSLLRVVNGILD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QDGKLTAIDYIGENGEILIANPSKQGKEGYRMFKFNKVFGTHSSQAEVFSDIQPLIRS
                                                                                                                                                                                                                                                                                                                                                                                                               RHHDRMPSRHILRPSRAAAGGIQAREGRIRPWGLRIRRLLPTLPP"
join(8072. .8086,9178. .9387,9474. .9671,12990. .13120,
14072. .14144,14960. .15376)
join(8072. .8086,9178. .9387,9474. .9671,12990. .13120,
10in(8072. .8086,9178. .9387,9474. .9671,12990. .13120,
14072. .14144,14960. .15376)
/gene="Nos7Maga014K08.2"
/note="Mypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="contains ESTs AU065754 (S10005), AU175140 (S10005) "
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/protein_id="BAC05580.1"
/db_xref="G1:21902031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               join(16191. .16218,17138. .17280)
/gene="OSJNBa0014K08.3"
join(16191. .16218,17138. .17280)
/gene="OSJNBa0014K08.3"
3405. .3547,5098. .5199,6055.
/gene="OSJNBa0014K08.1"
                                                               'note="hypothetical protein"
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                                                                                                                              /protein_id="BAC05577.1"
/db_xref="GI:21902028"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="BAC05578.1"
/db_xref="GI:21902029"
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/db_xref="G1:21902030"
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Submitted (27-SEP-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 222256)
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Submitted (15-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
                                                                                                                                                                                                           Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
   Rattus norvegicus clone CH230-179K4, *** SEQUENCING IN PROGRESS
                                                                               ACI3482.2 GI:25007228
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 222256)
Rat Genome Sequencing Consortium.
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Rat Genome Sequencing Consortium.
                        ***, 2 unordered pieces. AC134482
                                                                                                                                                                                   Rattus norvegicus
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                                                                                                                                                                                                                                                                        Rattus.
DEFINITION
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AUTHORS
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Baylor Plaza, Houston, TX 77030, USA On Nov 15, 2002 this sequence version replaced gi:23334632. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   data.html).
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Consensus quality: 190050 bases at least Q40
Consensus quality: 194119 bases at least Q30
Estimated insert size: 204504; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 AGCCGGACGCAACTCCTTATCGGAACAGGACGCGCCTCCATATCAGCCGCGCGTTATCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.h NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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107900 222256: contig of 114257 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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    .222256
    /organism="Rattus norvegicus"

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Center clone name: CH230-179K4
------- Summary Statistics
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/db_xref="taxon:10116"
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end_sequence:BH303478"
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Matches 69; Conservative
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102157. .103191
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242793. .243887
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48655. .249752
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!46116. .248554
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Best Local Similarity 53.1%;
Matches 69; Conservative
        Direct Submission
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                                                      AC135655 270958 bp DNA linear HTG 20-NOV-2002
Rattus norvegicus clone CH230-6908, *** SEQUENCING IN PROGRESS ***,
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                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                   AC135655.2 GI:25138854
HTG; HTGS_PHASE1; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
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Direct Submission
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                                                                                                                                                                                                                                          Rattus norvegicus
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VKTYRKAGEDYKY FASPADAEI FEHELAYALLHQI FSFNSPVWFNVGTPQPQQVSACF
ILAVDDSMESILDWYKEEGMI FKGGSGAGLNI.SRI RSSKELLSSGGNASGPVSFMRGA
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HDVGLALIGPLRELDLYAXLRPASVYRAFDSLEDFEAAIAELREGRERPAVDDEDHE
DAGAERQGTDRGSGGTVEVPVPATVAD"
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VFPLPRQLVGDGELFVLKVVGDSMIEAAICDGDWVTVRRQPVAENGDIVAAMLDGEAT
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FEAWKMGVKALAIYRDNCKVGQPLSAKKKETEKAEVTAKTEATIREAVEKVVEYRPVR
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NCIMB 12804 or NRRL 8165.~synonym: Streptomyces
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db_xref="G1:29606111"
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/gene="nrd"
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/gene="lexA"
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                                                                 105760 AACTAGACCCGCTCCTCATCAGCTCAGTACATTCTCTCTGGGCCTGGACCCCTTCTATC 105819
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Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis
Nat. Biotechnol. 21 (5), 526-531 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AP005031 299550 bp DNA linear BCT 10-MAY-2003 Streptomyces avermitilis genomic DNA, complete genome, section
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This work was done in collaboration with Haruo Ikeda(*1), Jun Ishikawa (*2), Akiharu Hanamoto(*3), Chiqusa Takahashi(*3), Mayumi Shinose(*3), Hiroshi Horikawa(*4), Hidekazu Nakazawa (*4), Tomomi Osonoe(*4), Norihiro Kushida(*4), Hisashi Kikuchi(*4), Tadayoshi Shiba(*5), Yoshiyuki Sakaki(*6,*7), Masahira Hattori(*1,*7) and Satoshi Omura(*1,*3).

Final finishing process and all annotation were done by H. Ikeda and J. Ishikawa.
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Submitted (29-MAR-2002) Director-General of Biotechnology Center,
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*2 National Institute of Infectious Diseases
*3 The Kitasato Institute
*A National Institute of Technology and Evaluation
*5 School of Science, Kitasato University
*6 Institute of Medical Science, University of Tokyo
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Omura, S., Ikeda, H., Ishikawa, J., Hanamoto, A., Takahashi, C.,
Shinose, M., Takahashi, Y., Horikawa, H., Nakazawa, H., Osonoe, T.,
Kushida, N., Director-General of Biotechnology Center, Shiba, T.,
            AGCCGGACGCAACTCCTTATCGGAACAGGACGCGCCTCCATATCAGCCGCGCGTTATCTC
                                                                                                                            ATGCGCGTGACCGGACACGAGGCGCCCGTCCCGCTTATCGCGCCCTATAAATACAGCCCGC
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Proc. Natl. Acad. Sci. U.S.A. 98 (21), 12215-12220 (2001)
21477403
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Pollowing url is also available.
http://avermitilis.ls kitasato-u.ac.jp.
Location/Qualifiers
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Gaps

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33; Indels

Mismatches

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52; Conservative

Matches

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APSVPARAGATAASADSDGCSDAVDPAAPFAAASTVPSASRYPSABSPVTSABVSTATA
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ADLDSLARHYPARPHDTGIHLLIGGVADRGRGLGSTLLRAVADLVLDRRPSCARVVAE
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complement (8549 . 10609)
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QLQTAAGEFERAMELALPGRIEEI PEDLGYALMALRDAARTYISAIGATRDKSVQDED
AVRKQALASVESVHDVAERITNGSEWDVVWYERHDRFGASLRVAPMSVSGLLREKLFA
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AKHLSRPAROGDRADMLDELTELIQAAGGRTLGFSSWRAAQLAAEELRSRIPEFPIL
LQGEETLGELI KNFAADPETCLFGTLSLAWQCVPOEDSCQLVWDKI PFPRPDDELMS
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LKASLPDFWYTTDRNQVRRSLTAIDEAAKKTEVTEVTEVAEVTEEAAKESEGA"

COMPLEMENT (7376. . 8509)
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QAAAVENLLRCWVRENGLVAPDDGTLRIPLLATGTALLVPVHHWSPTGWHRFGLPYLA
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KRELHKOVENTRLLERGCLGEOWDAHPPEDFULVBDPAULAVDDGGGNFOFDDWIRHD
PFAPTDDVSCVAGLVSRPWPOPTBOPRPWRSRLARIIIRLAGRTGRPRGAVATEWF
LRYLEQVVRPVLWLDSEAGIALEAHQONTLLLLDPEGWPTGGRYRDNGCYYFRTSRA
ELEARLPGIGERSDTFVSDEVTDERFAYYLGINNVLGLIGAFGSQHLAEEQLLLAAFR
RFLADVATGPARLRTPLPTRLLDSPVLRCKANLLITRLHGLDELVGPVDTQSVYTTIAN
PLHS.
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AVFIDDRRARPADEPDLFLAAEQALLLCHPLHPTPKSREGLSEARARLYSPELRGSFA
LHWLAVAPPVLATNSAWTERGRPVPAEQLTARLAGDGLPMPDGFAALPLHPWQIREIR
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TPVKDAFTTELFRTLPAGLADRARVQFCGPAGTDAVEAFKLVRTATGRSGLLAFTGA
YHGMTAGALEASGGATDGRVARLPYPQDYRCPFGIGGERGAELGARWTESLLDDVKSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EHSGVVPDVMVLSKAIGGSLPLAVVVTRDDLDVWQPGÄHÄGTFRGNQLAMÄAGTATLA
YVERENLAERAQTIGARMLDQLRSLATEPFCVGSVGSVRGRGLMIGVBLVRAEBDREAVSP
GSGDFASLDTRGAGRPAAPELAAAVQRECLRRGLIVELGGRHASVVRLLPPLTISDB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tränslation="MPPTDASTDAEPATSADPARIAVSARSAADSEDTLELRLPDELV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MAVTKSAVASLKREAEGAHAAHEGILRRQSARESAARTYARALP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="SAV2465"
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/transl_table=
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CDS

CDS

18.2%; Score 32.2; DB 1; Length 299550; 61.2%; Pred. No. 80;

Query Match Best Local Similarity

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PI RADOMIR CREVENJAKOV, MARK DICKSON, SNEZANA GEORGE LAMSON, RADOJE
PI RADOMIR CREVENJAKOV, MARK DICKSON, SNEZANA DRWANAC, IVAN LABAT,
PI DENA LESHKOWITZ, DAVID KITA, VERONICA GARCIA, LEE WILLIAM JONES,
PI SIRGIT STACHE CRAIN
PC CLANIS,09, COTKI4/47, CO7KI6/18, C12NI/15, C12NI/19, C12NI/21 PC
,C12NS/00, C12Q1/68,
PC CLANIS/00, C12NS/00
CC n = A,T,C or G
FH Key
FT min
                                                                              128986 CCTCCACCGAACCGGACGCGTCGCCCTTGATGATGAGGTTGAGTTCCTGCACCAGACCGG 129045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 921)
Williams, L.T., Becobedo, J., Innis, M.A., Garcia, P.D., Klinger, J.S., Reinhard, C., Giese, K., Randazzo, F., Kennedy, G.C., Pot, D., Kassam, A., Lamson, G., Drmanac, R., Crkvenjakov, R., Dickson, M., and Crain, B.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAT 17-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98
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Patent: JP 2002534055-A 2465 15-OCT-2002;
CHIRON CORP, HYSEQ INC
OS Homo sapiens (human)
PN JP 2002534055-A/2465
PD 15-OCT-2002
PP 13-MAY-1998 US 60/085426,15-MAY-1998 US 60/085537 PR 14-MAY-1998 US 60/08569,21-OCT-1998 US 60/105234 PR 27-OCT-1998 US 60/105877
PT LOUIS T WILLIAMS, JAIME ESCOBEDO, MICHAEL A INNIS, PABLO PI DOMINGUEZ GARCIA,
157 GGCAGCTGCGCACGCTGCCCACGCCGGTCTCCGCGCCTGCCCGGGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    921 bp DNA Human gene and gene expression product V. BD221352
                                                                                                                                                                                                                 129046 CCTTGAGGCCTCGTCCAGGTTCTC 129070
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Location/Qualifiers
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                                                                                                                                                                 118 ACACGAGGCGCCCGTCCCGCTTATC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BD221352.1 GI:33031122
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Homo sapiens (human)
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Matches 68; Conserve
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BD221352/c
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AUTHORS
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JOURNAL
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SOURCE
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kgletsckkkkgaeeraesaalkryelaadrmamgakaapycaddgrwstlsgqqled
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="mosammnpaagysslonsekylidpndfyglalspctvfkogl
Fmemsglrifalltapkptepkravihrskrnvclkacadgsvnlakalnslrmplcm
vkimaelnnasaprogmyrkrfeftcylgnvvsctkcksacligallhfykmdpkcvg
Evthllikaedvykesncakmktvnklcpkagmckgknpicnf"
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vgmnetrislakkggcoppinnihesytnspesfynkviweneykpivyigtdsgeee
eilievslupkykefrapadapletgpay"
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                                                                                                                                                                 complement(1. .738)
/note="ORF 1; ph Op3/Ac8; major occlusion body protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="late expression factor 2"
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/note="ORF 3; lef-2 Op6/Ac6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2647. .3657
/note="ORF 6; bro Ac2"
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FVAPSPQATQTPSFRQTFAAPSPVFAESPQPTRAFPTPEGTLSRGAADEFEYRAGTSV
                                                                                                                                                                                                                                                                                                                                                                                                                                      Barrett,J.W., Krell,P.J. and Arif,B.M.
Characterization, sequencing and phylogeny of the ecdysteroid UDP-glucosyltransferase gene from two distinct nuclear polyhedrosis viruses isolated from Choristoneura funiferana
J. Gen. Virol. 76 (Pt 10), 2447-2456 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The putative LEF-1 proteins from two distinct Choristoneura fumiferana multiple nucleopolyhedroviruses share domain homology to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Canada
On or before Oct 8, 2003 this sequence version replaced gi:1117788,
gi:2581770, gi:1754838, gi:4092491.
Location/Qualifiers
                                                                                                                                                                    AY327402 131158 bp DNA circular VRL 08-OCT-2003
Choristoneura fumiferana defective nucleopolyhedrovirus complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 13243 to 14241)
Barrett,J.W., Lauzon,H.A., Mercuri,P.S., Krell,P.J., Sohi,S.S. and
Arif,B.M.
                                                                                                                                                                                                                                                                                                                                Choristoneura fumiferana defective nucleopolyhedrovirus (CEDEFNPV) Choristoneura fumiferana defective nucleopolyhedrovirus Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lauzon, H. A. M., Jamleson, P. B., Krell, P. J. and Arif, B. M.
Direct Submission
Submitted (20-JUN-2003) Molecular Virology, Great Lakes Forestry
Centre, 1219 Queen St. E., Sault Ste. Marie, Ontario PGA 2E5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Li,X., Barrett,J., Pang,A., Klose,R.J., Krell,P.J. and Arif,B.M. Characterization of an overexpressed spindle protein during a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modecular analysis of the p48 gene of Choristoneura fumiferana multicapsid nucleopolyhedroviruses CfMNPV and CfDEFNPV J. Gen. Virol. 80 (Pt 7), 1833-1840 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 (bases 80268 to 81693)
Li,X., Lauzon,H.A., Sohi,S.S., Palli,S.R., Retnakaran,A. and
Arif,B.M.
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Virus Genes 13 (3), 229-237 (1996)
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Virology 268 (1), 56-67 (2000)
20149221
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EINCHAPLETRGASRVQAFFALDSLEFPDNMTDSLQVTMGRRPHFVRGYALTHYANVF
DPTIKLDGWWYNKFCVLTYWYRIIRGTVPAELITRLQNVVTKYIKPEYDESNNALAMG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LVCWTLFVVFQPQ1YKNGHVPVLDARYRDYDRNSLCWSN1VSDTYEVHDTNAIRTDFN
VYRHDFVKKVCKORRENHDEPTVRHONQOCALIMVNMYATVLQFWNMYVQRKENRYK
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PIVQSSSSPNSPDSGIDYDIPQPFYSVPNKVVCKYLCKTHATLCA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RY FACTSINMTQLAGROHFDRIL PGQSDRINU FDRILGREVINVATNTFRRSWDELLEDG
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VTRVRHVVPGDRSSVCASIVDGLDTTTASHRFRVECVNTYTSIGNFSNNKLLCPSDTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="MLAQINYILQLVLHAALYTITLIAFVFSLMGTINYKYAFLLELN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MYRILIVLFLFALLYIVVWPFYQAYQHIQTAQHDYNDTLTDRMD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YIESVMRRRHYVPMEALPSVQFDTNLGTLAGETLKCMSVPLYVTEIDLPFFDCTQVCE
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Pred. No. 94;
0; Mismatches 5; Indels 0:
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Best Local Similarity 87.5%;
Matches 35; Conservative
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Db 125416 CTAATAACGCCTATAAATACAGCCCGCTGCGATCTGGTAA 125377
Search completed: May 10, 2005, 05:52:43
Job time : 1077.29 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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177
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	Adq48575 OpiE2 pro	Aav62487 O. pseudo	Aa161306 p2ZOp2F e	Adq48539 Viral vec	Adq48576 Viral vec	Aaa02474 Human col	Abl18801 Drosophil	Abl27503 Drosophil	Abl27502 Drosophil	Abl18800 Drosophil	Aad64735 Human car	Adt47065 Bacterial	Adi45632 Plant iso	Abd14088 Pseudomon	Ads89385 Oligonucl	Ads89483 Oligonucl	Abk31430 Signal tr	Abl70389 Chemicall	Aas61341 Human gen	Adf83430 Bread whe
	Q I	ADQ48575	AAV62487	AAL61306	ADQ48539	ADQ48576	AAA02474	ABL18801	ABL27503	ABL27502	ABL18800	AAD64735	ADT47065	AD145632	ABD14088	ADS89385	ADS89483	ABK31430	ABL70389	AAS61341	ADF83430
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,	* Query Match Length DB	560	564	2773	5038	141	921	1268	1342	3448	3600	29169	1404	657	1710	3107	3501	6107	6107	6107	1370
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	Score	177	177	177	175.4	41	32	30.8	30.8	30.8	30.8	30.8	30.6	30	30	30	30	30	30	30	29.8
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Abl19245 Drosophil Abl19244 Drosophil Aba01209 Human col Ad44569 Bacterial Abd1376 Pseudomon Ach89781 Human gen Aas70780 DNA encod Aas51490 Pseudomon Aca19456 Prokaryot Ad856860 Bacterial Abd13439 Pseudomon Abd13439 Pseudomon Abd13439 Pseudomon Abd13639 Pseudomon Abd13639 Pseudomon Abd13639 Pseudomon Abk90730 cDNA enco Ach43165 Bacterial Aca45469 Human neu Abk90731 cDNA enco Ach43165 Bacterial Aca45469 Human neu Abk90731 cDNA enco Ad443165 Prokaryot Ad127170 Human gen Ada66376 Human LFN	GNMENTS recombinant virus; eration; gene expression inhibition; moter.	Madden K, Frimpong K, Franke KE; ng all or a portion of one or more two or more recombination sites that each other, useful as gene therapy.
ABL19245 ABL19244 AAA01209 ADT45695 ADT45695 ADT45695 ADT45696 AAS70780 AAS70780 AAS70780 ABD13493 ABD13493 ABK90731 ABK90731 ABK90731 ADT43165 ADT445469 ADT43165 ADT43165 ADA63958 ADA63958 ADA63958 ACM45469 ADM63958 ACM45469 ADM63958 ACM45469 ADM63958 ACM43958	H E0	od S, omprisi
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	standard; D 04 (first moter DNA s tor; recomb on-defectiv apy vector; ied.	
œœ <i>`</i> œ`ø`ø`ø`ø`ø`ø`ø`ø`ø`ø`ø***************	7 1 878 80048575 standard, DNA ADQ48575; 09-SEP-2004 (first er OpIE2 promoter DNA sec viral vector, recombir replication-defective gene therapy vector; o Unidentified.	TRUE W RECENT HEADED AND THE
888888888888888888888888888888888888888	RESULT 1 ADQ48575 sta XX AC ADQ48575; XX XX XX XX XX XX XX XX XY XX XX XX XX	OL - 10 D OL - 1
00000000000000000000000000000000000000	ULT 1 48575 ADC44 ADC44 09-S1 OPIE: viral repla gene Unid	29-J. 18-J. 18-J. 19-W. 19-WEL (INV (BEN) (MAD) (FRI) (FRI) (FRI) (FRI) WPI;
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The invention comprises a nucleic acid molecule consisting of all or a portion of one or more viral/baculoviral genomes and further containing at least two recombination sites that do not substantially recombine with each other. One or more of the recombination sites is capable of undergoing recombination with a compatible recombination site in the presence of one or more proteins active in lambda recombination. The nucleic acid of the invention replicates in prokaryotic and eukaryotic cells. The nucleic acid of the invention is useful for constructing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TATCGGAACAGGACGCGCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention
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                                                                                                                                                                                                                                                                                                                                                                                      recombinant virus, generating replication-defective particles, preventing/inhibiting the expression of one or more genes in an organism, and are useful as gene therapy vectors. The nucleic acid of the invention is also useful for producing and expressing fusion polypeptides. The present DNA sequence represents the OpIEZ promoter that was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     475 CGAGGCGCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 CGAGGCGCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 560 BP; 144 A; 156 C; 116 G; 144 T; 0 U; 0 Other;
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                              Disclosure; Fig 16; 555pp; English
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Matches 177; Conservative
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28-JAN-1998;
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19-JAN-1999
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that comprises: (i) prokaryotic origin of replication; (ii) insect that comprises: (i) prokaryotic origin of replication; (ii) insect to promoter having homology to, and capable of functioning as, an immediate early baculovius promoter; (iii) prokaryotic promoter sequence, and (iv) selectable marker capable of conferring resistance to a bleomycin, (iii) in insect and prokaryotic cells respectively. The vectors can be used to stably transform (especially insect) cells with heterologus on be, useful to allow study of gene expression and direct expression of heterologus gene products e.g. commercially important proteins. They are especially useful to allow expression of the heterologus compercially expecially useful to allow expression of the heterologus compension of the heterologus compension of the heterologus compension of the heterologus contains are derivatives in insect cells. They enable transformation of insect cell insect cells allow strains of particular proteins. Shuttle vectors further comprising DNA transposable elements defining a transposon can be compensed to optimise heterologus protein expression and facilitate selection of desired transformants. (Updated on 17-OCT-2003 to standardise OS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGAGGCGCCCGTCCCGCTTATCGCCGCTATAAATACAGCCCGCAACGATCTGGTAAA 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GTCTTATCGTGACAGGACGCCAGCTTCCTGTTGCTAACCGCAGCGGACGCAACTCCT
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expression and produce commercially important proteins
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                                                                                 Claim 10; Page 82; 121pp; English
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16-NOV-2001; 2001US-0331575P.
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Matches 177; Conservative (
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                                                                                                                             The invention relates to immunogenic analogues of multimeric proteins bench as immunogenic variants of interleukin 5 (ILE) and tumour necrosis factor alpha (TMF, TMFalpha) and methods for production of immunogenic analogues. The immunogenic analogue is useful for preparing a composition for treating inflammatory diseases, e.g., arthritis. It is also used in gene therapy. The present sequence is p220p2F expression vector for insect cells. This sequence is used to illustrate the method of the
                                                                                                                                                                                                                                                                                                                                       TATCGGAACAGGACGCCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACA 120
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                                                                           preparing a
                                                                                                                                                                                                                                                                                                                                                                                 CGAGGCGCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 177
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                                                                          New immunogenic analogue of a polymeric protein, useful for por
composition for treating inflammatory diseases e.g. arthritis
                                                                                                                                                                                                                                                  Length 2773;
                                Mouritsen S;
                                                                                                                                                                                                                             Sequence 2773 BP; 669 A; 750 C; 673 G; 681 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                viral vector; recombination site; recombinant virus;
                                                                                                                                                                                                                                                  100.0%; Score 177; DB 9; 100.0%; Pred. No. 3.8e-48;
                               Voldborg B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viral vector-related plasmid - pIB/V5-His-DEST
                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                         Disclosure; Page 195-196; 196pp; English.
                                Bratt T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADQ48539 standard; DNA; 5038 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002US-0396335P.
2002US-0398617P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-NOV-2002; 2002US-0427231P
24-MAR-2003; 2003US-0456496P
03-JUN-2003; 2003US-0474940P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JUL-2003; 2003WO-US022437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                             Best Local Similarity .vv. Matches 177; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INVITROGEN CORP
                               Nielsen FS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BENNETT R P.
WELCH P J.
HARWOOD S.
           MOURITSEN S
                                                   WPI; 2003-449558/42
 VOLDBORG B.
                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MADDEN K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2004009768-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JUL-2002;
26-JUL-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JAN-2004
                                Klysner S,
                                                                                                                                                                                                         invention
                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADQ48539;
                                                                                                                                                                                                                                                  Query Match
          MOUR/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BENN/)
(WELC/)
(HARW/)
(MADD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (INNI)
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portion of one or more viral/baculoviral genomes and further containing at least two recombination sites that do not substantially recombining each other. On or more of the recombination sites that do not substantially recombine with each other. We are more of the recombination sites is capable of undergoing recombination with a compatible recombination site in the presence of one or more proteins active in lambda recombination. The nucleic acid of the invention replicates in prokaryotic and eukaryotic cells. The mucleic acid of the invention is useful for constructing a recombinant virus, generating replication-defective particles, preventing/inhibiting the expression of one or more genes in an organism, and are useful as gene therapy vectors. The nucleic acid of the invention is also useful for producing and expressing fusion polypeptides. The present DNA sequence represents a plasmid that invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 TATCGGAACAGGACGCCCTCCATATCAGCCGCGTTATCTCATGCGCGTGACCGGACA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  411 TATCGGAACAGGACGCGCCTCCATATCAGCCGCGCGTATCTCATGCACGTGACCGGACA 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        351 Grerrarcereacadeacaccaderrecrererrecraceaccaccadeaccaacreer 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                  Novel nucleic acid molecule comprising all or a portion of one or more viral genome and further comprising two or more recombination sites that do not substantially recombine with each other, useful as gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 CGAGGCGCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            replication-defective particle generation; gene expression inhibition; gene therapy vector; ds; plasmid; recombination region.
Franke KE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GTCTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viral vector-related plasmid pIB/V5-His-DEST recombination region #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         471 CGAGGCGCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 12; Length 5038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5038 BP; 1342 A; 1178 C; 1198 G; 1320 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
    Frimpong K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 175.4; DB 12; Length
Pred. No. 1.5e-47;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               viral vector; recombination site; recombinant virus;
    Madden K,
                                                                                                                                                                                                                                                                                                                 Example 18; Page 395-403; 555pp; English.
    Harwood S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JUL-2002; 2002US-0396335P.
26-JUL-2002; 2002US-0398617P.
19-NOV-2002; 2002US-0427231P.
24-MAR-2003; 2003US-0456496P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADQ48576 standard; DNA; 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 176; Conservative
Welch PJ,
                                                                             WPI; 2004-132944/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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Sudduth-Klinger J;

(WELC/) (HARW/) (-INNI BENN/)

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76 CGCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACACGAGGCGCCCCGTCCC 135
                                                                                                                                                                                                                                                                                                                                                                                                                       Inbraries constructed from human colon cancer cell lines. The present linvention also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection che the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived. The polynucleotides sequences can be used in a method for detecting differentially expressed genes correlated with a cancerous state of mammalian cell. The polynucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of pre-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97 gecerchaanccacerrecerresiereseresesereseserreaggagesereses 38
                                                                                                                                                                                                                                                                                                      Polynucleotide library used to determine cancerous states of mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 decagéradeanécadéraderet cea edecederet es es decendes de estados de estados de estados de estados de esta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 GACGCCAGCTTCCTGTTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            metastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-
                                                                                                                      J, Innis MA, Garcia PD, Sudduth-Klinger Sandazzo F, Kennedy GC, Pot D, Kassam A; Crkvenjakov R, Dickson M, Dranac S, Labb Garcia V, Jones LW, Stache-Crain B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster genomic polynucleotide SEQ ID NO 7876.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 921 BP; 239 A; 214 C; 205 G; 223 T; 0 U; 40 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.1%; Score 32; DB 3; Length 921; ilarity 51.5%; Pred. No. 2.1; Conservative 0; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   negative breast cancer, lung cancer, and colon cancer
                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 989; 1097pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL18801 standard; DNA; 1268 BP.
98US-0105877P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136 GCTTATCGCGCC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pharmaceutical; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster.
                                                                                                                                                Reinhard C, Giese K,
Lamson G, Drmanac R,
Leshkowitz D, Kita D,
                                                                                                                           Escopedo
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                                                                                                                                                                                                                                                      WPI; 2000-126369/11.
                                                 (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 68; Conserv
                                                                            (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200171042-A2
  27-OCT-1998;
                                                                                                                           Williams LT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-SEP-2001.
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  g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             portion of one or more viral/baculoviral genomes and further containing at least two recombination sites that do not substantially recombine with each other. One or more of the recombination sites is capable of undergoing recombination with a compatible recombination site in the presence of one or more proteins active in lambda recombination. The nucleic acid of the invention replicates in prokaryotic and eukaryotic cells. The nucleic acid of the invention is useful for constructing a recombinant virus, generating replication-defective particles, preventing/inhibiting the expression of one or more genes in an organism, and are useful for producing and expressing fusion polypeptides. The invention is also useful for producing and expressing fusion polypeptides. The present DNA sequence represents a recombination region of a plasmid that was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                        Novel nucleic acid molecule comprising all or a portion of one or more viral genome and further comprising two or more recombination sites that do not substantially recombine with each other, useful as gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; colon cancer; tumour; diagnosis; gene expression product; probe; detection; cancerous state; metestatais; identification; breast cancer; coestrogen receptor-positive breast cancer; therapy; coestrogen receptor-negative breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                         Franke KE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human colon cancer cell line polynucleotide sequence SEQ ID NO:2465.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention comprises a nucleic acid molecule consisting of all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 23.2%; Score 41; DB 12; Length 141; l Similarity 100.0%; Pred. No. 0.0014; 41; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                         Madden K, Frimpong K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 141 BP; 43 A; 36 C; 27 G; 34 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              137 CTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 41
                                                                                                                                                                                                                                                            Harwood S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 17; 555pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA02474 standard; cDNA; 921 BP
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98US-0085537P.
98US-0085696P.
98US-0105234P.
  03-JUN-2003; 2003US-0474940P.
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                                                    INVITROGEN CORP.
                                                                                                                                                                                                                                                         Welch PJ,
                                                                         BENNETT R P. WELCH P J. HARWOOD S.
                                                                                                                                                                                                                                                                                                        WPI; 2004-132944/13.
                                                                                                                                                   (MADD/) MADDEN K.
(FRIM/) FRIMPONG K.
(FRAN/) FRANKE K E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-MAY-1998;
15-MAY-1998;
15-MAY-1998;
21-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09958675-A2
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                                                                                                                                                                                                                                                            Bennett RP,
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Query Match

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RESULT 6 AAA02474/c

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ABL27502;
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                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                        The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                        657 Acaacaderricegrigaaggreeceacaageggereeragreericerriggeggeereegg 716
                                                                                                                                                                                                                                                                                                                                                      92
                                                                                                              solated nucleic acid detection reagent for detecting 1000 or more from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                     17 ACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGC
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                  ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster genomic polynucleotide SEQ ID NO 33982.
                                                                                                                                                                                                                                                                                                            Score 30.8; DB 4; Length 1268;
Pred. No. 5.6;
0; Mismatches 47; Indels 0
                                                                                                                                                                                                                                                                                         Sequence 1268 BP; 295 A; 336 C; 360 G; 277 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                            77 GCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACACG 122
                                                                                                                                                                                                                                                                                                                                                                                                                 717 GTTGGCACATTGGCCATACAAATCCTCAAGTCCCAGAAAGTACAAG 762
                                                                                                                                                       Claim 1; SEQ ID NO 7876; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                 47; Indels
                                                                       Myers EW;
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                                                                      Li PWD,
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 23-MAR-2001; 2001WO-US009231
                    23-MAR-2000; 2000US-0191637P,
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                                                                                             17.4%;
ilarity 55.7%;
Conservative
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11-JUL-2000; 2000US-00614150
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                                                                      Adams M,
                                                                                          WPI; 2001-656860/75
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                                                  (PEKE ) PE CORP NY.
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                                                                                                                                                                                                                                                                                                                       Local Similarity
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                                                                                                              isolated
                                                                                                                                  interactions
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                                                                      Venter JC,
                                                                                                                                                                                                                                                                                                             Query Match
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Matches
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-AB130511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB57377-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               731 ACAACAGCTICCGGIGGAGGIGCCCACAAGCGGGICCTAGICCTIGGCGGCTCCGGIGGC 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92
New isolated nucleic acid detection reagent for detecting 1000 or more
genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 ACCCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGC
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                                                                                                                                                      Claim 1; SEQ ID NO 33982; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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11-JUL-2000; 2000US-00614150.
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Best Local Similarity 55.7%;
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-656860/75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
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genes from Drosophila and for elucidating cell signaling and cell-cell
discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB7737-ABB772072). The sequence data for this patent did not form part of the parinced specification, but was obtained in electronic format directly
                                                                                                                                                                                                                             17 ACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGC
                                                                                                                                                                                             Gaps
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                                                                                                                                                  Score 30.8; DB 4; Length 3448; Pred. No. 7.1; 0; Mismatches 47; Indels 0;
                                                                                                                                                                                                                                                                                                                                             1607 GTTGGCACATTGGCCATACAAATCCTCAAGTCCCAGAAAGTACAAG 1562
                                                                                                                                                                                                                                                                                                        77 GCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACACG 122
                                                                                                                Sequence 3448 BP; 894 A; 817 C; 801 G; 936 T; 0 U; 0 Other;
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11-JUL-2000; 2000US-00614150.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to novel recombinant carcinoma-associated protein (GAP) useful for screening a bioactive agent capable of binding to carcinoma associated (GA) protein and for evaluating the effect of a candidate carcinoma drug. The invention also describes the use of novel compositions for use in screening methods and provides compositions and methods associated with altered expression of TBX21 in cancer. Suitable cancers which can be diagnosed or screened by the invention includes actinar cell carcinoma, fibrosarcoma, Kaposi's sarcoma, breast cancer and thairy cell leukaemia. The present sequence is human carcinoma-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70
16
                                                                                                                                                                                                                                                                                                     Carcinoma-associated protein; CAP; acinar cell carcinoma; fibrosarcoma;
Kaposi's sarcoma; breast cancer; Hairy cell leukaemia; human; ds.
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17 ACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TBX21 protein, useful for screening a bloactive agent capable of bir to carcinoma associated protein, and for evaluating the effect of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 29169 BP; 5725 A; 7553 C; 7224 G; 8641 T; 0 U; 26 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        recombinant carcinoma-associated protein such as mouse
                                                                                            GTTGGCACATTGGCCATACAAATCCTCAAGTCCCAGAAAGTACAAG 1562
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                                                                                                                                                                                                                                                                        (CA) gene TBX21.
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02-MAR-2001; 2001US-00798586.
08-NOV-2001; 2001US-00052482.
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61.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        candidate carcinoma drug.
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02-MAR-2001;
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Gaps

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Score 30.8; DB 4; Length 3600; Pred. No. 7.2; 0; Mismatches 47; Indels 0;

Query Match
Best Local Similarity 55.7%;
Matches 59; Conservative

Length 1404;

DB 13;

Query Match

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cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant disease resistance; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polynucleotide; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Goldman BS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 45503; 122pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen X,
                                                     ADT47065 standard; cDNA; 1404 BP
                                                                                                                                                                                                                Bacterial polynucleotide #21816.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-FEB-2003; 2003US-00369493
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                                                                                                                                                             (first entry)
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HINKLE G J.
SLATER S C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-061375/06.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2003233675-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHEN X.
                                                                                                                                                          02-DEC-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-DEC-2003
                                                                                                        ADT47065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria.
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(CHEN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GOLD/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HINK/)
RESULT 12
                   ADT47065

ADT47065

ADT47065

ADT4 ADT4

ADT4 ADT4

ADT4 ADT4

ADT7 ADT7

ADT
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New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.

The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to promote functional in a plant cell, where the promoter is positioned to provide for expression of a polymucleotide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property comprises transformed plant with the recombinant DNA construct and growing the transformed plant where the polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for producing plants with improved plant properties, e.g. improved cold, heat or drought tolerance, improved plant properties, e.g. improved cold, heat or drought tolerance, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polymuciecline used and the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at sequencials sequence.html.

Sequence 1404 BP; 236 A; 489 C; 454 G; 225 T; 0 U; 0 Other;

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                                                        99 ATCTCATGCGCGTGACCGGACACGAGGCGCCCGTCCCGCTTATCGCGCCCTATAAATACAG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a polynucleotide (or its complement, protein encoding fragment or reverse complement), comprising a nucleotide sequence encoding a polypeptide comprising an amino acid sequence involved in or associated with the biosynthesis of isoprenoids in a rice plant. Also included are an isolated polypeptide involved in or associated with the biosynthesis of isoprenoids in a plant, an expression
                                                                             464 ACCGCAAGGGCGTGAACGTGCCCGATGTGGTGCTGCCGCCTTGCCGCCTTTCGGCCAAGG 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  with isoprenoid
its, for targeted
                                                                                                                                                                                                                                                                                                                        isoprenoid biosynthesis; ss; isopentenyl diphosphate; IPP; dimethylallyl alcohol; DMAPP; short-chain plastid prenyltransferase; gibberellin; carotenoid; abscisic acid; tocopherol; plastoquinone; phylloquinone; mevalonate pathway; phytosterol; brassinosteroid; ubiquinone; monterpene; sesquiterpene; protein prenylation; chlorophyll;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotides and polypeptides associated with iso synthesis in plants, useful for producing transgenic plants, for gene disruption, as well as markers or probes.
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(atagiri F, Kreps J, Moughamer T, Provart N,
                              Indels
                             29;
                                                                                                                                                                                                                                                                                              Plant isoprenoid biosynthesis-associated DNA #6.
 Score 30.6; Di
Pred. No. 6.7;
                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 563; 117pp; English
                                                                                                                                                                                                               뮵
                                                                                                              159 CCCGCAACGATCTGGTA 175
                                                                                                                                          524 ACCGCGACGATCTGGAA 540
17.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-SEP-2001; 2001US-0325277P.
04-APR-2002; 2002US-0370620P.
04-APR-2002; 2002US-0370743P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-SEP-2002; 2002US-00259194
                                                                                                                                                                                                               ADI45632 standard; DNA; 657
               Best Local Similarity 62.3
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Katagiri F,
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COOPER B.
GLAZEBROOK J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LANGE B M.
GHASSEMIAN M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KREPS J.
MOUGHAMER T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-090562/09.
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                                                                                                                                                                                                                                                                                                                                                                                                  haeme; yield.
                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified.
                                                                                                                                                                                                                                                                    22-APR-2004
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Goff SA,
                                                                                                                                                                                                                                          ADI45632;
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(KREP/)
(MOUG/)
(PROV/)
(RICK/)
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(GOFF/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LANG/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhu T;
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cassette. The polypeptides and polymuclectides include those associated with the biosynthesis of isopenenyl diphosphate (IPP) and dimethylallyl alcohol (DWAPP), the biosynthesis of short-chain plastid prespirates of short-chain plastid prenyltransferases, the biosynthesis of gibberellins, the biosynthesis of archonida and/or abscisic acids, the biosynthesis of tocopherols. Distributions and/or phylloquinone biosynthesis, the mevalonate pathway, phytosterol and brassinosteroid metabolism, biosynthesis of ubiquinone, biosynthesis of monopherols. Distributions of monopherols, where the biosynthesis of monopherols, and corn homologues of some of the rice polymucleotides. The polymucleotides are useful for producing transgenic plants, where the polymucleotides are useful for producing transgenic plants, where the polymucleotides are useful for producing transgenic plants, where the polymucleotides are useful for producing of the invention, or in which the corresponding gene has been disrupted, e.g. to result in a loss, a decrease or an alteration in the function of the product encoded better quality product than the corresponding wild-type plant. The nucleic acid molecules are useful for targeted gene disruption, as well as markers and probes. Note if the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         506 reriegredecarecacacacacacacacacacrescrescanasacececesecece 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29 TGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGCGCCTCCATATCA 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     segdata.uspto.gov/sequence.html?DocID=20040010815. The present sequence is an isoprenoid biosynthesis- associated DNA included in the sequence listing but not mentioned anywhere else in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89 GCCGCGCGTTATCTCATGCGCGTGACCGCACACGAGGCGCCCGTCCCCGCTTATCGCGC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              446 GCCGCATGATTGCGTGTTCTCGTGCCGGGTCTCGACGGGGCCGGCTGGCCTCCCGCGC 389
cassette comprising the polynucleotide, a host cell comprising the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 16.9%; Score 30; DB 12; Length 657; I Similarity 53.4%; Pred. No. 8.9; 63; Conservative 0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 657 BP; 109 A; 257 C; 178 G; 113 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GENO-) GENOME THERAPEUTICS CORP.
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P-PSDB; ABO80517.
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Best Local Similarity
Matches 63; Conserv
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27-JUL-1998;
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The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therepay of pathological conditions, as molecular tragets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, of for the ability to bind a P. aeruginosa nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant or production of P. aeruginosa drugs, as templates for recombinant components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABD01397-CABD17967 represent P. aeruginosa polynucleotides of the invention. Note: The sequence data for this patent did not form part of the printed of the sequence of the printed of the sequence of the printed of the components of the printed of the components of the componen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 CCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACGAGGCGCCCGCTCCCGCTTA 140
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useful as molecular targets for diagnostics, prophylaxis and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Predicting responsiveness of a subject with breast cell proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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proliferative disorders comprises analyzing methylation pattern of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ss; cell proliferative disorder; breast; methylation; cytostatic; gene therapy; single nucleotide polymorphism; SNP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1710 BP; 380 A; 455 C; 526 G; 349 T; 0 U; 0 Other;
                        pathological conditions resulting from bacterial infection.
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Look MP,
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Schmitt M,
                                                                       Disclosure; SEQ ID NO 12692; 455pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Koenig T,
Schmitt A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADS89385 standard; DNA; 3107 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seqdata.uspto.gov/sequence.html
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07-JAN-2003; 2003DE-01000096.
17-APR-2003; 2003DE-01017955.
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Best Local Similarity 57.4
Matches 54; Conservative
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Nimmrich I,
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ADS89385/c
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of a subject with a cell proliferative disorder of the breast tissues to at the target comprising analysing the methylation pattern of a target nucleic acid by contacting at least one of the target nucleic acids in a biological sample obtained from the subject prior to or during treatment. The method of the invention has cytostatic activity, and may have a use in gene therapy. The set of oligomucleotides comprising at least two of the oligomers are useful for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) within the sequences. The methods, nucleic acid, oligomucleotide, and kit are useful for the treatment, characteriaation, classification and/or differentiation, of breast cell proliferative disorders. The method is also useful for the predicting the responsiveness of a subject with a cell proliferative disorders to a therapy. The present sequence is used in the exemplification of the invention.
                                                                                  The invention relates to a novel method for predicting the responsiveness
                        Claim 25; SEQ ID NO 401; 104pp; English.
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16.9%; Score 30; DB 13; Length 3107; 50.7%; Pred. No. 13; tive 0; Mismatches 70; Indels ( Sequence 3107 BP; 823 A; 120 C; 814 G; 1350 T; 0 U; 0 Other; Query Match Best Local Similarity 50.77 Matches 72; Conservative

2079 AACGCGAAACCACCCGCTCCTCCTCGCTCCAACGCCGCCGAAATAACCTCAACCGC 2020 2019 GAÁCCCGCGACTCTTCCTCATTTTAAACAACTTCCTTAACGCGCCCGAACAAACGACCCG 1960 66 GAACAGGACGCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACGAGG 125 6 ATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCG 65 126 CGCCCGTCCCGCTTATCGCGCC 147 g ઠ ઠે ò

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Search completed: May 10, 2005, 04:32:48 Job time : 201.559 secs

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Sequence 2371, Ap
Sequence 1101, Ap
Sequence 12370, A
Sequence 12097, A
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7028, Ap
621, App
2740, Ap
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Sequence 13193, A
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4921.273 Million cell updates/sec
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Sequence 5,
Sequence 12
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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-902-540-131
US-09-902-540-131
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US-09-252-991A-12323
US-09-252-991A-12323
US-09-252-991A-12323
US-09-126-121-22
US-09-126-121-5
US-09-126-121-5
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US-09-252-991A-14837
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Sequence 12692, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                     Sequence 219, App
Sequence 228, App
Sequence 15207, A
Sequence 17417, A
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14970, A
52474, Ap
52551, Ap
5635, Ap
3318, Ap
1048, Ap
1110, Ap
1154, Ap
1269, Ap
200, App
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Sequence 2371, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Highe, Gregory J.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
CURRENT PAPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-07-10
                                                 Sequence 2099,
Sequence 5615,
Sequence 1963,
Sequence 1963,
Sequence 1110,
Sequence 1154,
Sequence 200,
Sequence 100, P
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                    Sequence
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                                                                                                                                                                                                                                US-09-252-991A-193
US-09-252-991A-219
US-09-252-991A-228
US-09-99-016-15207
US-09-949-016-17417
                                                                US-09-902-540-5635
US-09-902-540-3318
US-09-902-540-1048
US-09-902-540-1110
US-09-902-540-1154
US-09-902-540-1154
US-09-902-540-1154
US-09-902-540-1269
US-09-902-540-1269
US-09-252-991A-200
US-10-105-319-1
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Pred. No. 2
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Best Local Similarity 57.4%;
Matches 54; Conservative
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US-09-902-540-2371
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Sequence 12370, Application US/09252991A

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;

TITLE OF INVENTION: ABENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPRENCE: 107196-136

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

PRIOR FILING DATE: 1998-07-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 GCCGGACGCAACTCCTTATCGGAACAGGACGCGCCTCCATATCAGCCGCGCGTTATCTCA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                368 GCCGGCAGTTCCTCGTCGTCTGGACCGGAGACACCTCCATCTTCCTGACGCGTGTCAACC 427
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APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Berry J.

APPLICANT: Glater, Steven C.

APPLICANT: Wiegand, Roger C.

APPLICANT: Wie
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Pred. No. 4.3;
0; Mismatches 47; Indels 0;
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Pred. No. 2.1;
0; Mismatches 47; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      105 TGCGCGTGACCGGACACGAGGCGCCCGTCCCGCTTATCGCGCCTA 149
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Best Local Similarity 55.2%;
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 55.2%;
Matches 58; Conservative
                                                                                                                                         TYPE: DNA; ORGANISM: Myxococcus xanthus US-09-902-540-2371
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SEQ ID NO 12370
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 2371
LENGTH: 1311
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US-09-902-540-1101/c
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Sequence 12223, Application US/09252991A
Facent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: UNMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR PLING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
NOMBER OF SEQ ID NOS: 33142
NUMBER OF SEQ ID NOS: 33142
LENGTH: 1551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AREUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 12097
                                                                                                                                                                                                                                                                         534 CGTCGCCTGCTGGCAGGGGCTGGTGTGGACGCCGATGCCCGCTTCGATACCGTGGTCGA 475
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                                                                                                       Length 585;
                                                                                                                                                                 54; Indels
                                                                                                          DB 4;
                                                                                                          Score 28.6; DB
Pred. No. 4.3;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12097, Application US/09252991A Patent No. 6551795
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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                                                                                                          16.2%;
ilarity 53.0%;
Conservative
                                                                                                          Query Match
Best Local Similarity
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US-09-252-991A-12323/c
                                  ; UKGANIGA: .....
US-09-252-991A-12370
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; ORGANISM: Pseudo:
US-09-252-991A-12323
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55 ACTCCTTATCGGAACAGGGCGCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGAC 114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT:
APPLICANT:
GEOGWAKI, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
TITLE OF INVENTION: Ligands and Uses Therefor
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.2%; Score 28.6; DB 3; Length 2091; 58.0%; Pred. No. 6.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: 3.5 inch, 1.44 Mb floppy disk IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENCE APPLICATION DATA:
APPLICATION NUMBER: US/09/126,121
FILING DATE: 30-Jul-1998
CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: Conley, Deirdre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P1084R1D1
TELECOMMINICATION INFORMATION:
TELEPHONE: 650/252-2066
TELEFAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P1084R1D1
                                                                                               P1084R1
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                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Human NRG3B2 (hNRGB2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 22, Application US/09126121
Patent No. 6252051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: WinPatin (Genentech)
                                        NAME: Conley, Deirdre L. REGISTRATION NUMBER: 36,487 REPERBUCE/DOCKET NUMBER: P10 TELECOMMUNICATION INFORMATION: 650/225-2066
                                                                                                                                                         INFORMATION FOR SEQ ID NO: 22 SEQUENCE CHARACTERISTICS: LENGTH: 2091 base pairs TYPE: Nucleic Acid STRANDEDNESS: Single
                    ATTORNEY/AGENT INFORMATION: NAME: Conley, Deirdre L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 2091 base pairs TYPE: Nucleic Acid STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1-2091
IDENTIFICATION METHOD:
OTHER INFORMATION:
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MEDIUM TYPE: 3.5 inc
                                                                                                                                                                                                                                                                                                                TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
CLASSIFICATION:
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US-09-126-121-22
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Sequence 12237, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

HORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION:

TORRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR PRILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 12237

LENGTH:: 2085
                                                                                                                                                            802 CGTCGCCTGCTGGCAGGGGCTGGTGTCGGACGCCGATGCCCGCTTCGATACCGTGGTCGA 861
                                                                                                                   29
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                                                                                                                 8 CGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGA
                                                                                                                                                                                                              68 ACAGGACGCCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACACG 122
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Patent No. 6121415
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
TITLE OF INVENTION: Ligands and Uses Therefor
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
                    Score 28.6; DB 4; Length 1551;
Pred. No. 5.8;
0; Mismatches 54; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16.2%; Score 28.6; DB 4; Length 2085; 53.0%; Pred. No. 6.3;
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                 ch 16.2%;
1 Similarity 53.0%;
61; Conservative (
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STATE: California
COUNTRY: USA
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Best Local Similarity 53.0
Matches 61, Conservative
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                                          Local Similarity
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                      Query Match
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                                                                 Matches
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Linear
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US-09-902-540-1239
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FEATURE:
                                                                                        RESULT 11
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                                                                                                                                                                                                                                                                                                                     115 CGGACACGAGGCGCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGG 173
                                                                                                                                                                                                                                                                                                                                                                507 dedecaccedereccearcedeceaeceaecedececececeaeceaeaeaeaeaeeee 565
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                                                                                                                                                                                     1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao TITLE OF INVENTION: ExbB Receptor-Specific Neuregulin Related TITLE OF INVENTION: Ligands and Uses Therefor NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEB: Genentech, Inc.
                                                                                                                                   Score 28.6; DB 3; Length 2091;
Pred. No. 6.3;
0; Mismatches 49; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.2%; Score 28.6; DB 3; Length 2502; 58.0%; Pred. No. 6.7; ive 0; Mismatches 49; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human NRG3B1 (hNRG3B1) /nucleic acid seq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: WinPatin (Generated)
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/899,437
FILING DATE: 24-Uul-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COALBY, Delidire L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: 19,084R1
TELEPHONE: 650/225-2066
Human NRG3B2 (hNRGB2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-899-437-5; Sequence 5, Application US/08899437; Patent No. 6121415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 650/952-9811
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 2502 base pairs TYPE: Nucleic Acid STRANDEDNESS: Single TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1 DNA way
CITY: South San Francisco
STATE: California
                                                                                                                                     16.2%;
58.0%;
                                                                                                                              Query Match
Best Local Similarity 58.04
Matches 69, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 58.0
Matches 69; Conservative
                     LOCATION: 1-2091
IDENTIFICATION METHOD:
OTHER INFORMATION:
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IDENTIFICATION METHOD:
OTHER INFORMATION:
NAME/KEY:
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US-09-126-121-22
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55 ACTCCTTATCGGAACAGGGCGCCTCCATATCAGCCGCGCGCTTATCTCATGCGCGTGAC 114
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115 CGGACACGAGGCGCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGG 173
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Patent No. 683347

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Stere, Steven C.

APPLICANT: Wiegand, Roger C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related TITLE OF INVENTION: Ligands and Uses Therefor NUMBER OF SEQUENCE: 23
ADDRESSED: ADDRESS:
ADDRESSE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
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Pred. No. 6.7;
0; Mismatches 49; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Human NRG3B1(hNRG3B1)/nucleic acid seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA: PTLING DATE: 30-Jul-1998 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P1084R1D1
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NAME: CONLey, Deirdre L.
REGISTATION UNDHER: 36,487
REFERENCE/DOCKET NUMBER: P1084
TELECOMMUNICATION INFORMATION:
TELEFHONE: 650/252-2066
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                          US-09-126-121-5
; Sequence 5, Application US/09126121
; Patent No. 6252051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.2%;
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CITY: South San Francisco
STATE: California
COUNTRY: USA
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TYPE: Nucleic Acid
STRANDEDNESS: Single
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Best Local Similarity 58.0
Matches 69; Conservative
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IDENTIFICATION METHOD:
OTHER INFORMATION:
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US-09-513-999C-27806
                                                                                                     US-09-513-999C-27806
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Sequence 13983, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-10-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FEBSESEQ FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6260 TTTTTTTGACGACACTCCACCCATCGATGTTGGTACCAGGGGGTGGAAACATCGAAATCA 6319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 TTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTAT 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
16.2%; Score 28.6; D:
Best Local Similarity 49.0%; Pred. No. 13;
Matches 76; Conservative 0; Mismatches
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49.3%; Pred. No. 20;
CURRENT APPLICATION NUMBER: US/09/902,540
                                        CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 1239

LENGTH: 25048

TYPE: DNA

ORGANISM: Myxococcus xanthus

US-09-902-540-1239
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LOCATION: (1)...(57320)
OTHER INFORMATION: n = A,T,C or G
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Matches 74; Conservative
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                                                         FAUCHAUT: Duras Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REPERROR: 59.US2.REG
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR SEQ ID NOS: 36681
SOUTHARE: Patent.pm
SEQ ID NO 27806
LENGTH: 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7217, Application US/09902540

Patent No. 6833477

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Hinkle, Gregory J.

APPLICANT: Hinkle, Roger C.

APPLICANT: Wiegand, Roger C.

TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REPERENCE: 38-10(18849)B

CURRENT APPLICATION NUMBER: US/09/902,540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
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15.9%; Score 28.2; D
Best Local Similarity 68.4%; Pred. No. 4.8;
Matches 39; Conservative 0; Mismatches
Patent No. 678361
GRNPDA: No. 6783961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 7217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: v=a or c or g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 54.3%;
Matches 57; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: m=a or c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: misc_feature
LOCATION: 197
OTHER INFORMATION: k=g or
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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1657 CAGGTGACGGGCTTCGCGGGTTGCTCCAGCCCAAACGCCGGAAGCCAGGGGGAGTAC 1716

g à d

Search completed: May 10, 2005, 07:29:35 Job time : 60.8508 secs

Sequence 50761, A
Sequence 35867, A
Sequence 44133, A
Sequence 65984, A
Sequence 22976, A
Sequence 7326, Ap
Sequence 7326, Ap
Sequence 22, App1
Sequence 22, App1

Sequence 563, App Sequence 303, App Sequence 10, Appl

Seguence :

Sequence 4094, Ap Sequence 72869, A

Sequence 22, Appl Sequence 22, Appl Sequence 22, Appl Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli

Sequence 40821, A Sequence 58, Appl Sequence 166, App Sequence 135441,

Sequence

Sequence 41603, A Sequence 33339, A Sequence 17146, A

Sequence 176225,

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Gaps

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Length 462;

309

32.2 32.2 30.6

175.4

4 7 7 110 110

Score

Result g 9

Title: Perfect score:

Sequence:

nucleic

Run on:

Scoring table:

Database

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61 TATCGGAACAGGACGCCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence:Promoter OTHER INFORMATION: sequence of the OpMNPV ie2 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-136-573A-5
US-10-136-573A-5
US-10-215-862-5
US-10-244-116-5
US-10-282-122A-33339
US-10-425-114-17146
US-10-425-115-176225
US-10-425-115-176225
US-10-425-115-40821
US-10-034-650-58
US-10-087-192-166
US-10-425-115-135441
US-10-425-115-1364
8 US-10-437-963-42126

8 US-10-437-963-55473

US-10-259-1944-563

7 US-10-221-613-303

7 US-10-221-613-303

7 US-10-275-311A-10

8 US-10-437-963-72869

8 US-10-437-963-35867

8 US-10-437-963-35867

8 US-10-437-963-35867

8 US-10-425-4034

8 US-10-369-463-35867

10S-10-369-463-35867

10S-10-369-463-35867

10S-10-369-44133

10S-10-812-242-4072

10S-10-369-493-32534

10S-09-817-665-22

10S-09-817-667-22

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Pred. No. 1.5e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Insect Expression Vectors
FILE REFERENCE: 80021-44
CURRENT APPLICATION NUMBER: US/09/896,888A
CURRENT APPLICATION NUMBER: US/09/896,888A
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US/09/048,911
PRIOR APPLICATION NUMBER: 60/049,946
PRIOR APPLICATION NUMBER: 60/049,946
PRIOR FILING DATE: 1997-03-27
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIn Ver: 2.0
SEQ ID NO 14
LENGTH: 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Scor.
100.0%; Pred. No. ...
0; Mismatches
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US-09-877-665-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 14, Application US/0989688BA Patent No. US20020116723A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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Matches 177; Conservative
                                            4627
29322
75839
1011
1623
    US-09-896-888A-14
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2538, Ap
1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 89, Appl
Sequence 127, App
Sequence 149, App
Sequence 2538, Ap
Sequence 1, Appli
Sequence 45503, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 126, App
Sequence 1, Appli
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                                                                                                                                                                 (without alignments)
2164.037 Million cell updates/sec
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Sequence 60,
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| cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubna/USO0_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pub
                                                                                                                                          May 10, 2005, 05:52:55 ; Search time 500.12 Seconds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
                       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-846-911-60
US-10-622-088-89
US-10-622-088-127
US-10-622-088-149
US-10-156-761-2538
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US-10-369-493-45503
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US-10-622-088-126
US-09-896-888A-1
                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                 5654200 seqs, 3057283753 residues
                                                                                                                                                                                                                          US-09-896-888A-1_COPY_351_527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published Applications NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                    nucleic search, using sw model
                                                                                                                                                                                                                                                                                                        IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length
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18.2
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LENGTH: 2773
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310 TATCGGAACAGGACGCCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACA 369
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                                                                                                                               121 CGAGGCGCCCGTCCCGCTTATCGCGCCTATAATACAGCCCGCAACGATCTGGTAAA 177
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                                                                                                                                                                                                                                                                                                                                                                                      Sequence 126, Application US/10622088

Publication No. US20040219516A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Benneth, Robert P.
APPLICANT: Benneth, Reneth
APPLICANT: Frimpong, Kenneth
APPLICANT: Primpong, Kenneth
APPLICANT: Will Constant Sequence
FILE REFERENCE: 0942.545007
CURRENT APPLICATION NUMBER: PCT/US03/22437
FRIOR APPLICATION NUMBER: US 60/396,335
FRIOR FILING DATE: 2002-07-18
FRIOR FILING DATE: 2002-07-28
FRIOR PILING DATE: 2002-07-28
FRIOR FILING DATE: 2002-07-28
FRIOR FILING DATE: 2003-01-24
FRIOR FILING DATE: 2003-01-34
FRIOR FILING DATE: 2003-03-44
FRIOR FILING DATE: 2003-03-44
FRIOR FILING DATE: 2003-03-324
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US-09-896-888A-1
; Sequence 1, Application US/09896888A
; Patent No. US20020116723A1
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Insect Expression Vectors
; FILE REPRENCE: 80021-44
; CURRENT APPLICATION NUMBER: US/09/896,888A
; CURRENT PILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US/09/048,911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: OPIE2 promoter sequence US-10-622-088-126
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ORGANISM: Unknown
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351 GTCTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCT 410
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                                                                                                                                                                                                                                                                                                                                                                             1 GICTIATCGIGACAGGACGCCAGCITCCIGIGITGCTAACCGCAGCGGACGCAACTCCT
                                                                                                                                                                                                                                                                                                                              Gaps
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Publication No. US20030185845A1
GENERAL INFORMATION:
APPLICANT: Pharmexa A/S
TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
FILE REPERENCE: PLO13DK00
CURRENT APPLICATION NUMBER: US/10/295,074
CURRENT FILING DATE: 2002-11-15
NUMBER OF SEQ ID NOS: 60
SOPTWARE: Patentin version 3.1
SEQ ID NO 600
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0
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                                                                                                                                                                                                                                                                        Length 564;
                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                          ; Score 177; DB 9;
; Pred. No. 1.5e-54;
0; Mismatches 0;
                            ,049,946
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LOCATION: (561)...(566)
CHERE INFORMATION: HindIII site
PEATURE:
NAME/KEY: misc_recomb
LOCATION: (573)...(578)
OTHER INFORMATION: Aval site
                                                                                                                                                                                                                                                                             Query Match

Best Local Similarity 100.0%;

Matches 177; Conservative 0
PRIOR FILING DATE: 1998-03-26
PRIOR PELLING DATE: 1997-03-27
PRIOR FILING DATE: 1997-03-27
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.0
LENGTH: 564
                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Orgyia pseudotsugata
US-09-896-888A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc recomb
LOCATION: (593)..(598)
OTHER INFORMATION: BamHI site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc recomb
LOCATION: (586)..(591)
OTHER INFORMATION: ECORI site
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LOCATION: (629)..(634)
OTHER INFORMATION: ClaI site
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OTHER INFORMATION: Clai
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LOCATION: (1156)..(1161)
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LOCATION: (625)..(630
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TATCGGAACAGGACGCCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          475 CGAGGCGCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 531
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US-10-846-911-60

i Sequence 60, Application US/10846911

j Publication No. US20040258660A1

i GENERAL INFORMATION:
    APPLICANT: KILSEN, Finn Stausholm
    APPLICANT: HILSEN, Finn Stausholm
    APPLICANT: HRAIT, Tomas
    APPLICANT: OLDBORG, Bjorn
    APPLICANT: OLDBORG, Bjorn
    APPLICANT: WURITSEN, Sozen
    TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
    TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
    TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
    TITLE OF INVENTION NUMBER: PC/10/046, 911
    CURRENT FILING DATE: 2004-05-14
    PRIOR FILING DATE: 2002-11-15
    PRIOR PILING DATE: 2001-11-16
    PRIOR APPLICATION NUMBER: PR 2001 01702
    PRIOR SEQ ID NOS: 60
    SOFTWARE: PALENTIN VERSION 3.1
    LENGTH: 2773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GTCTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCT
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                                                                                                                                                                                                                                                  COLORION: NCOL BLUE

NAME/KEY: misc_recomb

LOCATION: (2284)...(2289)

FEATURE:
NAME/KEY: misc_recomb

NAME/KEY: misc_recomb

CLOCATION: (2294)...(2299)

OTHER INFORMATION: Aval, Smal, and Xmal site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_recomb
LOCATION: (561)..(566)
OTHER INFORMATION: HindIII site
PEATURE:
                                                  NAME/KEY: misc recomb
LOCATION: (2128)..(2133)
OTHER INFORMATION: PstI site
FEATURE:
NAME/KEY: misc recomb
LOCATION: (2204)..(2209)
OTHER INFORMATION: NCOI site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KRY: misc recomb
LOCATION: (2551)..(2556)
COTHER INFORMATION: Apall site
US-10-295-074-60
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ORGANISM: Artificial sequence
OTHER INFORMATION: ApaLI site
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355 GTCTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCT 414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_recomb
LOCATION: (2294)..(2299)
OTHER INFORMATION: Aval, Smal, and Xmal site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 89, Application US/10622088
Publication No. US20040219516A1
GENERAL INFORMATION:
APPLICANT: Bennett, Robert P.
APPLICANT: Welch, Peter J.
APPLICANT: Harwood, Steven
APPLICANT: Frimpong, Kenneth
APPLICANT: Frimpong, Kenneth
APPLICANT: Franke, Kenneth
                                                                                                                                                                                                 NAME/KEY: misc recomb
LOCATION: (593)..(598)
OTHER INFORMATION: BamHI site
FEATURE:
NAME/KEY: misc recomb
LOCATION: (625)..(630)
OTHER INFORMATION: ClaI site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: misc_recomb
LOCATION: (1155)..(1161)
OTHER INFORMATION: Apall site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:

NAME/KEY: misc recomb

LOCATION: (2551)...(2556)

OTHER INFORWATION: Apail site
US-10-846-911-60
                                                                         FEATURE:
NAME/KEY: misc_recomb
LOCATION: (586)..(591)
OTHER INFORMATION: ECORI site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc recomb
LOCATION: (2204)..(2209)
OTHER INFORMATION: NCOI site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: misc_recomb
LOCATION: (2128)..(2133)
OTHER INFORMATION: PstI site
                            LOCATION: (573)...(578)
OTHER INFORMATION: Aval site
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NAME/KEX: misc recomb
LOCATION: (629\(\frac{7}{10}\)...(634)
OTHER INFORMATION: Clai site
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LOCATION: (2284)..(2289)
OTHER INFORMATION: Aval site
NAME/KEY: misc_recomb
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Gaps

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0; Indels

Length 147;

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FEATURE: OTHER INFORMATION: Recombination region of plB/V5-His-DEST
                                                                                                                                                                                                                                                Score 41; DB 18;
Pred. No. 8e-05;
                                                                                                                                                                                                                                             Query Match 23.2%; Score 41; DB Best Local Similarity 100.0%; Pred. No. 8e-Matches 41; Conservative 0; Mismatches
                                                                                                                               NAME/KEY: misc feature

LOCATION: (141)...(148)

CTHER INFORMATION: n may be any nucleotide

US-10-622-088-127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (141)...(142)
OTHER INFORMATION: n is a, c, g, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 149, Application US/10622088 Publication No. US20040219516A1 GENERAL INFORMATION:
                               TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bennett, Robert P. APPLICANT: Welch, Peter J. APPLICANT: Harwood, Steven
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Madden, Knut
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Best Local Similarity 100.
Matches 41; Conservative
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; LOCATION: (145)..(276)
US-10-622-088-149
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ORGANISM: Artificial
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ## APPLICANT: Harwood, Steven
## APPLICANT: Harwood, Steven
## APPLICANT: Madden, Knut
## APPLICANT: Madden, Knut
## APPLICANT: Franke, Kenneth E.
## TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
## FILE REFERENCE: 0942-5450007
## CURRENT APPLICATION NUMBER: US/10/622,088
## CURRENT FILING DATE: 2003-07-18
## PRIOR APPLICATION NUMBER: US 60/396,335
## RIUNG DATE: 2002-07-18
## PRIOR FILING DATE: 2002-07-26
## PRIOR FILING DATE: 2002-07-26
## PRIOR FILING DATE: 2002-11-19
## PRIOR FILING DATE: 2003-03-24
## RIUNG APPLICATION NUMBER: US 60/474,940
## PRIOR FILING DATE: 2003-03-24
## NUMBER OF SEQ ID NOS: 165
## SEQ ID NO 127
DB 18; Length 5038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 99.1%; Score 175.4; DB 10
Best Local Similarity 99.4%; Pred. No. 8.2e-54;
Matches 176; Conservative 0; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: pIB/VS-His-DEST
US-10-622-088-89
                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Bennett, Robert P. APPLICANT: Welch, Peter J.
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Gaps
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APPLICANT: Madden, Knut
APPLICANT: Franke, Kenneth
APPLICANT: Franke, Kenneth E.
TILE REFERENCE: 0942.545007
CURRENT APPLICATION WIMBER: US/10/622,088
CURRENT APPLICATION NUMBER: 2003-07-18
PRIOR APPLICATION NUMBER: PCT/US03/22437
PRIOR APPLICATION NUMBER: DC 60/396,335
PRIOR APPLICATION NUMBER: US 60/396,335
PRIOR PLILNG DATE: 2002-07-18
PRIOR FILING DATE: 2002-07-18
PRIOR PLILNG DATE: 2002-07-18
PRIOR PLILNG DATE: 2002-11-19
PRIOR PLILNG DATE: 2002-11-19
PRIOR PLILNG DATE: 2002-11-19
PRIOR PLILNG DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PALENTIN VERSE: US 60/474,940
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PALENTIN VERSE: 2003-06-03
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 149
LENGTH: 325
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 CTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 177
1 crrarcececcraraaracaeceecaacearereeraaa 41
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, OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 32.2; DB Pred. No. 0.22; 0; Mismatches
SQUENCE 5238, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OWURA, SATOSHI
APPLICANT: ISHIKAWA, UNN
APPLICANT: ISHIKAWA, UNN
APPLICANT: SHIKAWA, UNN
APPLICANT: SHIKAWA, UNN
APPLICANT: SHIKAWA, UNN
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SHIRA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, WASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OWURA, SATOSHI
APPLICANT: ISHIKAWA, UDN
APPLICANT: ISHIKAWA, UDN
APPLICANT: SHIKAWA, HIROSHI
APPLICANT: SHIRAY, HAROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, MASAHIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT PLING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-08-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Streptomyces avermitilis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
18.2%;
Best Local Similarity 61.2%;
Matches 52; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature LOCATION: (4187715)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(3138)
US-10-156-761-2538
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: ApplicAnt: Acoustic, David K.
APPLICANT: ApplicAnt: Acoustic, David K.
APPLICANT: ApplicAnt: Acoustic, David K.
APPLICANT: Mu, Wei
APPLICANT: Mu, Wei
APPLICANT: David Molecules and Other Molecules Associated With
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICAND NUMBER: US/10/437,963
CURRENT PILLIG DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 42126
SERGITH: 1116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Garegory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
CURRENT APPLICATION NUMBER: US 60/360,039
CURRENT FILING DATE: 2003-02-21
CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 45503
LENGTH: 1404
                                                                                                                                                                                         3129487 CCTCCACCGAACCGGACGCGTCGCCCTTGATGATGAGGTTGAGTTCCTGCACCACAGACCGG 3129546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99 ATCTCATGCGCGTGACCGGACACGAGGCGCCCGTCCCGCTTATCGCGCCCTATAAATACAG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 464 Accecaaeeecereaacereccearerecrecreccerricececerrrrceeceaaee 523
                                                                                                                             58 CCTTATCGGAACAGGACGCCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGG
   Length 9025608;
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                                                                  Indels
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62.3%; Pred. No. 0.74;
tive 0; Mismatches 29;
                                                              33;
DB 15;
Score 32.2; DB Pred. No. 0.78; 0; Mismatches
                                                                                                                                                                                                                                                                                                3129547 CCTTGAGGCCTCGTCCAGGTTCTC 3129571
                                                                                                                                                                                                                                                        118 ACACGAGGCGCCCGTCCCGCTTATC 142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 45503, Application US/10369493
Publication No. US20030233675A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Rhodobacter capsulatus
US-10-369-493-45503
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   Query Match
Best Local Similarity 61.2%;
Matches 52; Conservative
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Best Local Similarity
Matches 48; Conserva
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; Publication No. US20040029123A1
; GENERAL INFORMATION:
    APPLICANT: OLEK, ALExander
; APPLICANT: OLEK, ALExander
; APPLICANT: DIEFPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with Cell Cycle
; FILE REFRENCE: 5013.1004
; CURRENT APPLICATION NUMBER: US/10/221,613
; CURRENT FILING DATE: 2002-09-13
; DE 10019058.8
; DE 10019058.8
; DE 1001973.8
; DE 10043826.1
; PRIOR FILING
                                                     APPLICANT: Nicholas
APPLICANT: Nicholas
APPLICANT: Ricke, Darrell
APPLICANT: Ricke, Darrell
APPLICANT: Ricke, Darrell
APPLICANT: Ricke, Darrell
APPLICANT: Zhu, Tong
TITLE OF INVENTION: IDENTIFICATION AND CHARACTERIZATION OF PLANT GENES
FILE REFERENCE: 70029-NP
CURRENT APPLICATION NUMBER: US 60/325,277
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR APPLICATION NUMBER: US 60/370,743
PRIOR PILING DATE: 2002-04-04
PRIOR PILING DATE: 2002-04-04
PRIOR PLING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 662
SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
: SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89 GCCGCGCGTTATCTCATGCGCGTGACCGGACACGAGGCGCCCCGTCCCGCTTATCGCGC 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 30; DB 17; Length 65'
Pred. No. 1.1;
0; Mismatches 55; Indels
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2000-03-15
2000-04-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Triticum aestivum
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Best Local Similarity 53.4*
Matches 63; Conservative
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SEQ ID NO 303
LENGTH: 6107
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Sequence 55473, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: LA ROSA, Thomas J.

APPLICANT: Cao, Yondwei

APPLICANT: Too, Yondwei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT APPLICANTON NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

SEQ ID NO 55473

LEGITH: 2472
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                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                             Length 1116;
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                                                                                                                                                                                     Score 30.2; DB 18; Length Pred. No. 1; 0; Mismatches 53; Indels
                                                         , OTHER INFORMATION: Clone ID: PAT_MRT4530_45406C.1
US-10-437-963-42126
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US-10-437-963-55473
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LOCATION: (1)..(2472)
OTHER INFORMATION: unsure at all n locations
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; Publication No. US20040010815A1
; GENERAL INFORMATION:
    APPLICANT: Lange, Markus B.
    APPLICANT: Briggs, Steven P.
    APPLICANT: Cooper, Bret
    APPLICANT: Glazebrook, Jane
    APPLICANT: Glazebrook, Jane
    APPLICANT: Glazebrook, Jane
    APPLICANT: Glazebrook, Jane
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Best Local Similarity 55.1%;
Matches 59; Conservative (
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1 Similarity 53.9%;
62; Conservative
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ORGANISM: Oryza sativa
ORGANISM: Oryza sativa
                                                                                                                                                                                             Query Match
Best Local Similarity
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5019 GAACCCGCGAUTCTTCCTCATTTTAAACAACTTCCTTAACGCCCCGAACAAACGACCG 4960
                                      66 GAACAGGACGCGCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACGAGG 125
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126 CGCCCGTCCCGCTTATCGCGCC 147

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Search completed: May 10, 2005, 10:29:03 Job time : 510.12 secs

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/pna/US109A_COMB.seq:*
//pna/US109B_COMB.seq:*
//pna/US109C_COMB.seq:*
//pna/US110_COMB.seq:*
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pna/US6001_COMB.seq:*
pna/US6002_COMB.seq:*
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pna/US6019_COMB.seq:*
pna/US6020_COMB.seq:*
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/pna/US6023A_C
/pna/US6023B_C
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/cgn2_6/ptodata/1/pna/US6045_
/cgn2_6/ptodata/1/pna/US6046_
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/pna/US6025 (
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pna/US6027
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1001:
102:
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 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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117: /cgn2_6/ptodata/1/pna/US6047_COMB.seq:*
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123: /cgn2_6/ptodata/1/pna/US6052_COMB.seq:*
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125: /cgn2_6/ptodata/1/pna/US6052_COMB.seq:*
126: /cgn2_6/ptodata/1/pna/US6055_COMB.seq:*
127: /cgn2_6/ptodata/1/pna/US6056_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## UMMARIES

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No.	Score	Match	Length	DB	ID	Description
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7	177	100.0	9		-968-60-	e 14,
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4	177	100.0	560		-US03-22437-1	126,
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9	177	00	9	16	-09-048-911	e 1,
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~	e	8	492		-09-904-939-299	e 29963
21	32.4	8	19	46	-10-015-1	e 5182,
c 55	N	8	520		-10-015-127	e 514, A
23	N	œ	861		-09-620-392-2289	e 22894
24	N	ω.	861		-09-702-134-275	e 27502
25	N	8	861		-09-815-264-8137	equence 81375
c 26	32.2	18.2	3138	49	-10-156-761-2538	equence 2538,
27	2	8	56		10-156-761-1	ce 1, A
~	32	ω.	921		-09-313-292-246	2465,
c 29		œ.	2	62	-10-779-543-856	8561,
30	ä	۲.	418	27	-09-606-977-59	59093
	31.4	ζ.	Н	83	-60-141-233-5909	59093
	31.4		2	36	9-837-604A-433	43377
	31.4	7	2	36	-09-837-604B-433	43377
	31.4		S	88	-60-197-872	e 40261
	0	17.4	9	27	-09-614-150-2544	equence 25442
	0	17.4	1268	27	-09-614-150	e 25442
	ö	17.4	26	86	-60-173-464-210	equence 21087
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	0	17.4	26		-60-191-681-2017	equence 20170
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41	ö	17.4	34		-09-614-150A-384	equence 38495
	。	17.4	m		-60-191-637-381	equence 3812
•	30.8	17.4	4	27	-09-614-150-3849	equence 38494
4	。	17.4	3448		-09-614-15	equence 3
c 45		17.4			37-3812	equence 381

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OTHER INFORMATION: Description of Artificial Sequence:Promoter
OTHER INFORMATION: sequence of the OpMNPV ie2 gene
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the OpMNPV ie2 gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 177; DB 16;
Pred. No. 1.3e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Insect Expression Vectors
FILE REFERENCE: 80021-44
FULRERENERICE: 80021-44
FULRERY APPLICATION NUMBER: US/09/896,888
CURRENT APPLICATION NUMBER: US/09/896,888
CURRENT FILING DATE: 2001-06-29
FRIOR APPLICATION NUMBER: US 09/048,911
FRIOR APPLICATION NUMBER: US 60/049,946
FRIOR APPLICATION NUMBER: US 60/049,946
FRIOR FILING DATE: 1997-03-27
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 14
LENGTH: 462
                                           APPLICANT: The University of British Columbia TITLE OF INVENTION: Insect Expression Vectors FILE REFERENCE: 80021-44.
CURRENT APPLICATION NUMBER: US/09/048,911
CURRENT FILING DATE: 1998-03-26
EARLIER APPLICATION NUMBER: US 60/049,946
EARLIER APPLICATION NUMBER: US 60/049,946
FARLIER ON DATE: 1997-03-27
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIn Ver. 2.0
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; GENERAL INFORMATION:
Sequence 14, Application US/09048911 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 177; Conservative
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LENGTH: 462
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TYPE: DNA
ORGANISM: Unknown
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310 TATCGGAACAGGACGCGCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACA 369
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GENERAL INFORMATION:

APPLICANT: Invitrogen Corporation

TITLE OF INVENTION: Viral Vectors Containing Recombination Sites

TILE REFERENCE: 0942.545PC07

CURRENT APPLICATION NUMBER: PCT/US03/22437

CURRENT FILING DATE: 2003-07-18

PRIOR APPLICATION NUMBER: US 60/396,335

PRIOR FILING DATE: 2002-07-26

PRIOR APPLICATION NUMBER: US 60/496,496

PRIOR PILING DATE: 2002-11-19

PRIOR PILING DATE: 2003-11-19

PRIOR PILING DATE: 2003-10-16

SRIOR APPLICATION NUMBER: US 60/474,940

PRIOR PILING DATE: 2003-06-03

NUMBER OF SEQ ID NOS: 146

SEQ ID NO 126

LENGTH: 560
                                                121 CGAGGCCCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA
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CTHER INFORMATION: Description of Artificial Sequence:Promoter:
CTHER INFORMATION: sequence of the OpMNPV ie2 gene
US-09-896-888A-14
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                                                                                                                                                                                                       Sequence 14, Application US/0999688A

GENERAL INFORMATION:

APPLICANT The University of Eritish Columbia
TITLE OF INVENTION: Insect Expression Vectors
FILE REPERENCE: 80021-44

CURRENT APPLICATION NUMBER: US/09/048,911

PRIOR APPLICATION NUMBER: US/09/048,911

PRIOR FILING DATE: 1998-03-26

PRIOR FILING DATE: 1998-03-27

NUMBER OF SEQ ID NOS: 50

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 14

LENGTH: 462
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ORGANISM: Artificial Sequence
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ORGANISM: Unknown
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355 GTCTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCT 414
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APPLICANT: Frimpong, Kenneth
APPLICANT: Frimpong, Kenneth
TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
FILE REFERENCE: 0942.545000.
FILE REFERENCE: 0942.545000.
CURRENT PILING DATE: 2003-07-18
CURRENT PILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/396,335
PRIOR FILING DATE: 2002-07-18
PRIOR PILING DATE: 2002-07-18
PRIOR PRIOR APPLICATION NUMBER: US 60/427,231
PRIOR PILING DATE: 2002-07-26
PRIOR PILING DATE: 2003-011-19
PRIOR PILING DATE: 2003-011-19
PRIOR PILING DATE: 2003-011-19
PRIOR PILING DATE: 2003-011-19
PRIOR PILING DATE: 2003-013-24
PRIOR PILING DATE: 2003-013-24
SPRIOR PILING DATE: 2003-013-24
SPRIOR PILING DATE: 2003-013-24
SPRIOR PILING DATE: 2003-05-05
NUMBER OF SEQ ID NOS: 165
SEQ ID NOS: 165
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100.0%; Pred. No. 1.3e-44;
tive 0; Mismatches 0;
                                                                                                                                                                     Query Match
100.0%; Score 177; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.3e-44;
Matches 177; Conservative 0; Mismatches 0;
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, OTHER INFORMATION: OpIE2 promoter sequence PCT-US03-22437-126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 126, Application US/10622088 GENERAL INFORMATION:
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Matches 177; Conservative
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US-09-896-888A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 177; DB 16; Best Local Similarity 100.0%; Pred. No. 1.3e-44; Matches 177; Conservative 0; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION: Insect Expression Vectors
FILE REPRENCE: 80021-44
CURRENT APPLICATION NUMBER: US/09/896,888
CURRENT APPLICATION NUMBER: US 09/048,911
PRIOR APPLICATION NUMBER: US 09/048,911
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1997-03-27
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIn Ver. 2.0
                                                             APPLICANT: The University of British Columbia TITLE OF INVENTION: Insect Expression Vectors FILE REPERBRES. 80021-44: US/09/048,911 CURRENT APPLICATION NUMBER: US/09/048,911 CURRENT FILING DATE: 1998-03-26 EARLIER APPLICATION NUMBER: US 60/049,946 EARLIER APPLICATION NUMBER: US 60/049,946 FARLIER OF SEQ ID NOS: 50 SOFTWARE: Patentin Ver. 2.0
                 Sequence 1, Application US/09048911 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                            TYPE: DNA; ORGANISM: Orgyia pseudotsugata
US-09-048-911-1
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; ORGANISM: Orgyia pseudotsugata
US-09-896-888-1
                                                                                                                                                                                                                                                            SEQ ID NO 1
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LENGTH: 564
US-09-048-911-1
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351 Grerrardereacadeaceceaecricererereraceaaceceaececaacece 410
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TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
FILLE REFERENCE: P1013DK00
CURRENT APPLICATION NUMBER: US/10/295,074
CURRENT PILLING DATE: 2002-11-15
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin version 3.1
LENGTH: 2773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 564;
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100.0%; Pred. No. 1.3e-44;
tive 0; Mismatches 0;
Sequence 1, Application US/09896888A;
GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION: Insect Expression Vectors
FILE REFERENCE: 80021-44
CURRENT APPLICATION NUMBER: US/09/048,911
FRIOR FILING DATE: 2001-06-29
FRIOR FILING DATE: 1998-03-26
FRIOR FILING DATE: 1998-03-26
FRIOR FILING DATE: 1997-03-27
NUMBER: OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-295-074-60; Sequence 60, Application US/10295074; GENERAL INFORMATION:
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LOCATION: (561)..(566)
OTHER INFORMATION: HindIII site
                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Orgaia pseudotsugata
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OTHER INFORMATION: ECORI site
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LOCATION: (593)..(598)
OTHER INFORMATION: BamHI site
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LOCATION: (573)..(578)
OTHER INFORMATION: Aval site
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Best Local Similarity 100.
Matches 177; Conservative
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NAME/KEY: misc recomb
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355 GTCTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCT 414
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                                                                     OTHER INFORMATION: p2ZOp2F expression vector for insect cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                    LOCATION: (561)..(566)
OTHER INFORMATION: HindIII site
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LOCATION: (629]...(634)
OTHER INFORMATION: ClaI site
FEATURE:
NAME/KEY: misc_recomb
LOCATION: (1156)...(1161)
OTHER INFORMATION: Apall site
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LOCATION: (2294)..(2299)
OTHER INFORMATION: Aval, Smal,
  TYPE: DNA
ORGANISM: Artificial sequence
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NAME/KRY: misc_recomb
LOCATION: (593). (598)
OTHER INFORMATION: BamHI site
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LOCATION: (2551)...(2556)
OTHER INFORMATION: ApaLI site
US-10-846-911-60
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LOCATION: (573)..(578)
OTHER INFORMATION: Aval site
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NAME/KEY: misc_recomb
LOCATION: (625)..(630)
OTHER INFORMATION: ClaI site
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LOCATION: (2284)..(2289)
OTHER INFORMATION: Aval site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc recomb
LOCATION: (2128)..(2133)
OTHER INFORMATION: Pstl site
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LOCATION: (2204)..(2209)
OTHER INFORMATION: NCOI site
                                                                                                                                                                                                                                                                                                                          LOCATION: (586)..(591)
OTHER INFORMATION: ECORI
                                                                                                                                                                                                                                                                                                     NAME/KEY: misc recomb
LOCATION: (586)..(591)
                                                                                                                NAME/KEY: misc recomb
LOCATION: (561)..(566
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NAME/KEY:
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APPLICANT: NIELSEN, Finn Stausholm
APPLICANT: NIELSEN, Finn Stausholm
APPLICANT: BRATT, Tomas
APPLICANT: BRATT, Tomas
APPLICANT: WOLLBORG, Bjorn
APPLICANT: WOURTSEN, Soren
TITLE OF INVENTAON: NOVEL IMMUNGENIC MIMETICS OF MULTIMER PROTEINS
FILE REFERENCE: 674542-2018
CURRENT APPLICATION NUMBER: US/10/846,911
CURRENT PILING DATE: 2004-05-14
PRIOR PILING DATE: 2002-11-16
PRIOR PILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-11-16
PRIOR FILING DATE: 2001-11-16
SPRIOR FILING DATE: 2001-11-16
SUFFWARE: PARENTIN NUMBER: 60
SOFFWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: misc_recomb
LOCATION: (2294)..(2299)
OTHER INFORMATION: Aval, Smal, and Xmal site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 60, Application US/10846911 GENERAL INFORMATION:
                                                                                                                                                    FEATURE:
NAME/KEY: misc_recomb
LOCATION: (1155)..(1161)
OTHER INFORMATION: Apall site
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LOCATION: (2551)...(2556)
OTHER INFORMATION: ApaLI site
US-10-295-074-60
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NAME/KEY: misc_recomb
LOCATION: (2284)..(2289)
OTHER INFORMATION: Aval site
                                                              FEATURE:
NAME/KEY: misc_recomb
LOCATION: (629)..(634)
OTHER INFORMATION: Clai site
                                                                                                                                                                                                                                                                          NAME/KEY: misc recomb
LOCATION: (2128)..(2133)
OTHER INFORMATION: PstI site
AME/KEY: misc recomb
ACATION: (625)..(630)
WHER INFORMATION: Clal site
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COCATION: (2204)..(2209)
THER INFORMATION: Ncol site
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US-10-846-911-60
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99.1%;
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                                                                                                                                                                                                              Best Local Similarity 99.4
Matches 176; Conservative
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                                            TYPE: DNA
ORGANISM: Artificial
FEATURE:
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Best Local Simi
Matches 41;
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                        5038
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SEQ ID NO 89
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                      LENGTH:
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                                                    PAPLICANT: Invitrogen Corporation
TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
FILE REFERENCE: 0942.545PC07
CURRENT APPLICATION NUMBER: PCT/US03/22437
CURRENT PILING DATE: 2003-07-18
PRIOR PELICATION NUMBER: US 60/396,335
PRIOR FILING DATE: 2002-07-26
PRIOR PLING DATE: 2002-07-26
PRIOR PLING DATE: 2002-07-26
PRIOR PLING DATE: 2002-11-19
PRIOR PLING DATE: 2002-11-19
PRIOR PLING DATE: 2003-03-24
PRIOR PLING DATE: 2003-03-24
PRIOR PLING DATE: 2003-03-24
PRIOR PLING DATE: 2003-03-24
PRIOR FILING DATE: 2003-03-34
PRIOR FILING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 146
SOFTWARE: PARLENT VERSION 3.2
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APPLICANT: Frimpong, Kenneth
APPLICANT: Frimpong, Kenneth E.
TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
FILE REFERENCE: 0942.5450007
CURRENT FILING DATE: 2003-07-18
FRIOR APPLICATION NUMBER: US/10/622,088
PRIOR APPLICATION NUMBER: US 60/396,335
PRIOR PILING DATE: 2002-07-18
PRIOR PLILING DATE: 2002-07-18
PRIOR PLILING DATE: 2002-07-26
PRIOR PLILING DATE: 2002-07-26
PRIOR PLILING DATE: 2002-07-26
PRIOR PLILING DATE: 2002-07-26
PRIOR PLILING DATE: 2003-03-49
PRIOR PLILING DATE: 2003-03-49
PRIOR PLILING DATE: 2003-03-6456,496
PRIOR PLILING DATE: 2003-03-60-03
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  Sequence 89, Application PC/TUS0322437
GENERAL INFORMATION:
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Madden, Knut
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LENGTH: 5038
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JAPPLICANT: INVIENTION: Viral Vectors Containing Recombination Sites
FILE OF INVENTION: Viral Vectors Containing Recombination Sites
FILE REFREENCE: 0942.545F0.

CURRENT APPLICATION NUMBER: PCT/US03/22437

CURRENT FILING DATE: 2003-07-18

PRIOR APPLICATION NUMBER: US 60/396,335

PRIOR FILING DATE: 2002-07-26

PRIOR FILING DATE: 2002-07-26

PRIOR FILING DATE: 2002-11-19

PRIOR PRILING DATE: 2003-03-24

PRIOR PRILING DATE: 2003-03-24

PRIOR FILING DATE: 2003-03-24

PRIOR FILING DATE: 2003-03-24

PRIOR FILING DATE: 2003-03-24

SROIN FILING DATE: 2003-03-24

SROIN FILING DATE: 2003-03-24

SROIN FILING DATE: 2003-03-24

SROIN FILING DATE: 2003-03-24

PRIOR FILING DATE: 2003-03-24

PRIOR FILING DATE: 2003-03-24

PRIOR FILING DATE: 2003-04-03

NUMBER OF SEQ ID NOS: 146

SEQ ID NO 127
                                                                                            Score 175.4; DB 58; Length 5038; Pred. No. 5.5e-44;
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                                                                                                                                                           1; Indels
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100.0%; Pred. No. 0.036;
tive 0; Mismatches 0
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; LOCATION: (141)...(148)
; OTHER INFORMATION: n may be any nucleotide
PCT-US03-22437-127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 127, Application PC/TUS0322437 GENERAL INFORMATION:
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) OTHER INFORMATION: pIB/V5-His-DEST
US-10-622-088-89
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Gaps

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Query Match 23.2%; Score 41; DB 58; Length 325; Best Local Similarity 100.0%; Pred. No. 0.04; Matches 41; Conservative 0; Mismatches 0; Indels
                                                    FEATURE: OTHER INFORMATION: Recombination region of pIB/V5 His DEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137 CTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 177
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                                                                                                         FEATURE:
NAME/KEX: misc_feature
LOCATION: (141)..(142)
OTHER INFORMATION: n is a, c, g, or
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                                                                                                                                                                                                                                                ; NAME/KEY: CDS
; LOCATION: (145)..(276)
US-10-622-088-149
                          ORGANISM: Artificial
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CURRENT APPLICATION NUMBER: US/10/622,088
CURRENT FILING DATE: 2003-07-18
PRIOR PILING DATE: 2003-07-18
PRIOR PILING DATE: 2003-07-18
PRIOR PILING DATE: 2002-07-18
PRIOR PILING DATE: 2002-07-18
PRIOR PILING DATE: 2002-07-18
PRIOR PILING DATE: 2002-11-19
PRIOR PILING DATE: 2002-11-19
PRIOR PILING DATE: 3002-11-19
PRIOR PILING DATE: 3003-03-24
PRIOR PILING DATE: 3003-03-24
PRIOR PILING DATE: 3003-03-24
PRIOR PILING DATE: 3003-03-24
                                APPLICANT: Frimpong, Kenneth
APPLICANT: Franke, Kenneth E.
TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
THE REFERENCE: 0942.545000/005/
CURRENT APPLICATION UNBER: US/10/622,088
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OTHER INFORMATION: Recombination region of pIB/V5-His-DEST
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CCATION: (141)...(148)
US-10-622-088-127
                                                                                                                                                                                  CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: PCT/US03/22437
PRIOR PILING DATE: 2003-07-18
PRIOR PLILING DATE: 2003-07-18
PRIOR PILING DATE: 2003-07-18
PRIOR PILING DATE: 2002-07-8
PRIOR PILING DATE: 2002-07-26
PRIOR PILING DATE: 2002-07-26
PRIOR PILING DATE: 2003-11-19
PRIOR PILING DATE: 2003-11-19
PRIOR PILING DATE: 2003-03-24
PRIOR PILING DATE: 2003-05-05
PRIOR PILING DATE: 2003-06-03
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ORGANISM: Artificial Sequence
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SEQ ID NO 149
LENGTH: 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bennett, Robert P. APPLICANT: Welch, Peter J. APPLICANT: Harwood, Steven APPLICANT: Madden, Knut
Harwood, Steven
Madden, Knut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 127
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Sequence 2371, Ap Sequence 2371, Ap Sequence 26107, A Sequence 1101, Ap Sequence 96240, A Sequence 6584, Ap Sequence 518, App Sequence 518, App
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Sequence 38495, A
Sequence 38494, A
Sequence 25441, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 35, Appl
Sequence 35, Appl
Sequence 1, Appli
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Sequence 401, App
Sequence 499, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 22, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 60, Appl
                                                                                                                    May 10, 2005, 05:51:35 ; Search time 436.346 Seconds (without alignments) 834.449 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                            1 gtcttatcgtgacaggacgc......gcccgcaacgatctggtaaa 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pending Patents_NA New:*

1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
2: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*
3: /cgn2_6/ptodata/1/pna/USO6_NEW_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/USO7_NEW_COMB.seq:*
5: /cgn2_6/ptodata/1/pna/USO7_NEW_COMB.seq:*
6: /cgn2_6/ptodata/1/pna/USO1_NEW_COMB.seq:*
7: /cgn2_6/ptodata/1/pna/USO1_NEW_COMB.seq:*
8: /cgn2_6/ptodata/1/pna/USO1_NEW_COMB.seq:*
9: /cgn2_6/ptodata/1/pna/USO1_NEW_COMB.seq:*
9: /cgn2_6/ptodata/1/pna/USO1_NEW_COMB.seq:*
10: /cgn2_6/ptodata/1/pna/USO1_NEW_COMB.seq:*
11: /cgn2_6/ptodata/1/pna/USO1_NEW_COMB.seq:*
12: /cgn2_6/ptodata/1/pna/USO1_NEW_COMB.seq:*
13: /cgn2_6/ptodata/1/pna/USO1_NEW_COMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                            18797578
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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0 US-11-097-143-38495

0 US-11-097-143-25441

PCT-USO5-07924-3

1 US-11-075-185-35

PCT-USO5-07924-1

US-11-075-185-3

US-11-075-185-3

US-11-075-185-3

US-11-075-185-1

US-11-075-185-1

US-11-0517-441-491
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US-11-097-143-26108
US-11-097-143-26107
US-11-031-175-1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-11-031-175-1101
US-10-703-032-96240
US-10-703-032-52910
US-10-450-763-6584
                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-11-035-787-22
                                                                                                                                                                                                                                                                                                                                                9398789 seqs, 1028555566 residues
                                                                                                                                                                                                US-09-896-888A-1_COPY_351_527
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Maximum Match 100%
Listing first 45 summaries
                                                                                - nucleic search, using sw model
                                                                                                                                                                                                                                                                                  IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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1703
2091
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1789
3915
13579
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229.8
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                                                                                OM nucleic
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                                                                                                                        Run on:
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Sequence 37529, A	US-10-972-079-37529	σ	009	15.4	27.2	45	
•	US-11-031-175-6433	11	549	15.4	27.2	44	Ü
	US-11-033-545-647	11	200918	15.5	27.4	43	O
Sequence 711, App	US-11-033-545-711	11	188504	15.5	27.4	4	J
Sequence 1, Appli	US-11-109-593-1	10	67323	15.5	27.4	41	
Sequence 1, Appli	PCT-US05-13243-1	-	67323	15.5	27.4	40	
Sequence 36, Appl	US-11-075-185-36	1	5679	15.5	27.4	39	
Sequence 36, Appl	PCT-US05-07924-36	~	5679	15.5	27.4	38	
Sequence 5, Appli	US-11-109-593-5	10	5643	15.5	27.4	37	
Sequence 5, Appli	PCT-US05-13243-5	~	5643	15.5	27.4	36	
Sequence 27145, A	US-11-097-143-27145	10	5314	15.5	27.4	32	O
Sequence 1430, Ap	US-10-450-763-1430	œ	1707	15.5	27.4	34	
Sequence 27146, A	US-11-097-143-27146	10	816	15.5	27.4	33	
Sequence 82054, A	US-10-703-032-82054	σ	601	15.5	27.4		Ü
Sequence 621, App	US-11-031-175-621	11	5588	15.7	27.8	31	
Sequence 7028, Ap	US-11-031-175-7028	11	2208	15.7	27.8	30	
Sequence 26385, A	US-10-703-032-26385	0	1200	15.7	27.8	53	
	US-10-703-032-28994	σ	579	15.7	27.8	. 58	J
Sequence 82313, A	US-10-703-032-82313	σ	200	15.7	27.8	: 27	υ
Sequence 674, App	US-11-031-175-674	Ξ	3612	15.9	28.5	c 26	J
Sequence 7217, Ap	US-11-031-175-7217	Ξ	2892	15.9	28.2	25	
Seguence 14117, A	US-10-450-763-14117	œ	2225	15.9	28.2	. 24	O
Sequence 11844, A	US-60-659-397-11844	13	215013	16.2	28.6	c 53	•
Sequence 1239, Ap	US-11-031-175-1239	Ξ	25048	16.2	28.6	22	
Sequence 5, Appli	US-11-035-787-5	1	2502	16.2	28.6	21	

## ALIGNMENTS

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Sequence 60, Application US/10939107

APPLICANT: Pederren, Hans Rudolf

APPLICANT: Pederren, Louise Henriette

APPLICANT: Pederren, Louise 100-10

CURRENT APPLICATION NUMBER: US/10/939,107

CURRENT APPLICATION NUMBER: PEDOR-09-10

PRIOR PILING DATE: 2003-03-11

PRIOR PILING DATE: 2003-03-11

PRIOR PILING DATE: 2002-03-11

PRIOR PILING DATE: 2002-03-11

PRIOR PILING DATE: 2002-03-11

PRIOR FILING DATE: 2003-03-11

PRIOR FILING PRIOR DAT
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657 ACAACAGCTTCCGGTGGAGGTGCCCACAAGCGGGTCCTAGTCCTTGGCGGCTCCGGTGGC 716
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                                                                                                                                                                                                                                                                                                                                                                                                                               17 ACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
TITLE OP INVENTION: DROSOPHILA GENES.
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 ACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGC
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                                                                                                                                                                                                                                                                                                                      Length 1268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77 GCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 GCCTCCATATCAGCCGCGTTATCTCATGCGCGTGACCGGACACG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                717 GTTGGCÁCATTGGCCATACAAATCCTCAAGTCCCAGAAAGTÁCAAG 762
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                                                                                                                                                                                                                                                                                                                   DB 10;
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Pred. No. 4.8;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT FILING DATE: 2005-04-04

FRIOR APPLICATION NUMBER: 60/157,832

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-19

PRIOR FILING DATE: 1999-10-19

PRIOR FILING DATE: 1999-10-19

PRIOR FILING DATE: 1999-10-28

PRIOR FILING DATE: 1999-11-12

PRIOR PILING DATE: 2000-01-12

PRIOR FILING DATE: 2000-01-12

PRIOR FILING DATE: 2000-01-12

PRIOR FILING DATE: 2000-01-2

PRIOR PILING DATE: 2000-02-24

PRIOR FILING DATE: 2000-03-23

NUMBER OF SEQ ID NOS: 43008

SEQ ID NO 34495
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 25442
LENGTH: 1268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 38495, Application US/11097143 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                   17.4%;
55.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Venter, J. Craig
                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                           ; ORGANISM: DROSOPHILA
US-11-097-143-25442
                                                                                                                                                                                                                                                                                                                                          Similarity
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; ORGANISM: DROSOI
US-11-097-143-38495
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Best Local &
                                                                                                                                                                                                          TYPE: DNA ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                        Matches
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TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DROSOPHILA GENES.

TITLE OF INVENTION: DROSOPHILA GENES.

TITLE OF INVENTION: DROSOPHILA GENES.

CURRENT APPLICATION NUMBER: US/11/097,143

CURRENT FILING DATE: 2005-04-04

PRIOR APPLICATION NUMBER: 60/150,191

PRIOR APPLICATION NUMBER: 60/160,191

PRIOR FILING DATE: 1999-10-19

PRIOR FILING DATE: 1999-10-28

PRIOR FILING DATE: 1999-11-28

PRIOR APPLICATION NUMBER: 60/161,932

PRIOR FILING DATE: 1999-11-12

PRIOR PRILING DATE: 1999-11-28

PRIOR PRILING DATE: 1999-11-12

PRIOR PLILING DATE: 1999-11-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  355 GICTIAICGIGACAGGACGCCAGCIICCIGIGIIGCIAACCGCAGCCGGACGCAACICCI 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TATCGGAACAGGCGCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          415 TATCGGAACAGGCGCCTCCATATCAGCCGCGCTTAICTCATGCGCGTGACCGGACA 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 CGAGGCGCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GTCTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCT
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 177; DB 7,
Best Local Similarity 100.0%; Pred. No. 1e-44;
Matches 177; Conservative 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_recomb
LOCATION: (2294)..(2299)
OTHER INFORMATION: Aval, Smal, and Xmal site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 25442, Application US/11097143
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/175,693
FILING DATE: 2000-01-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/184,831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; NAME/KEY: misc_recomb
; LOCATION: (2551)..(2556)
; OTHER INFORMATION: Apals site
US-10-939-107-60
                                                                                                                                                                 NAME/KEY: misc_recomb
LOCATION: (1156)..(1161)
OTHER INFORMATION: Apall site
                                                                                                                                                                                                                                                                                NAME/KEY: misc recomb
LOCATION: (2128)..(2133)
OTHER INFORMATION: PStI site
                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc recomb
LOCATION: (2204)..(2209)
OTHER INFORMATION: NCOI site
                                                       NAME/KEY: misc recomb
LOCATION: (629)..(634)
OTHER INFORMATION: ClaI site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc recomb
LOCATION: (2284).. (2289)
OTHER INFORMATION: Aval site
FEATURE:
OTHER INFORMATION: ClaI site
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엄 ò 셤 8 790

92

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TYPE: DNA ORGANISM: DROSOPHILA
                                                                                                                                                                                                                                       US-11-097-143-25441
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APPLICANT: Venter, U. Craig
APPLICANT: Let al.
ITILE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
ITILE OF INVENTION: DROSOPHILA GENES.
ITILE OF INVENTION: DROSOPHILA GENES.
ITILE OF INVENTION: DROSOPHILA GENES.
FILE REPERENCE: CLOOO728
CURRENT PILING DATE: 2005-04-04
RIOR APPLICATION NUMBER: 60/157,832
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR PAPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR FILING DATE: 1999-11-12
PRIOR PRILICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
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                                                      APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: BETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 ACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGC
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0; Mismatches
                                                                                                                                                                                         TILLE REFERENCE: CL000728

CURRENT APPLICATION NUMBER: US/11/097,143

CURRENT FILING DATE: 2005-04-04

PRIOR APPLICATION NUMBER: 60/157,832

PRIOR FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: 60/161,932

PRIOR APPLICATION NUMBER: 60/161,932

PRIOR FILING DATE: 1999-10-19

PRIOR FILING DATE: 1999-10-12

PRIOR FILING DATE: 1999-11-12

PRIOR FILING DATE: 1999-11-12

PRIOR FILING DATE: 1999-11-12

PRIOR FILING DATE: 1999-11-12

PRIOR FILING DATE: 2000-01-28

PRIOR PILING DATE: 2000-01-2

PRIOR APPLICATION NUMBER: 60/175,693

PRIOR PILING DATE: 2000-01-12

PRIOR FILING DATE: 2000-01-12

PRIOR FILING DATE: 2000-01-12

PRIOR FILING DATE: 2000-01-2

PRIOR FILING DATE: 2000-01-2

PRIOR FILING DATE: 2000-01-2

PRIOR FILING DATE: 2000-02-24
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 38494
LENGTH: 3448
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GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
Sequence 38494, Application US/11097143
GENERAL INFORMATION:
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Matches 59; Conservative
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US-11-097-143-25441/c
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; Sequence 35, Application PC/TUSO507924
; GENERAL INFORMATION:
APPLICANT: JULIEN, BRYAN
; APPLICANT: JULIEN, BRYAN
; TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMBRUTICINS
; FILE REFERENCE: 010099.03
; CURRENT APPLICATION NUMBER: PCT/USO5/07924
; CURRENT FILING DATE: 2005-03-17
; PRIOR PLING DATE: 2004-03-08
; RIOR FILING DATE: 2004-03-08
; SOFTWARE: PatentIn version 3.3
; SOFTWARE: PatentIn version 3.3
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APPLICANT: REID, RALPH
TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMBRUTICINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 GCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACACG 122
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Pred. No. 5.2;
0; Mismatches 47;
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Pred. No. 6.6;
0; Mismatches
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR FILING DATE: 2000-02-24
PRIOR PPLING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 25441
LENGTH: 3600
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TYPE: DNA
ORGANISM: Sorangium cellulosum
                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 55.7%;
Matches 59; Conservative
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Best Local Similarity 53.3%;
Matches 88; Conservative
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SEQ ID NO 1
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Sequence 1, Application PC/TUSOS07924

Sequence 1, Application PC/TUSOS07924

APPLICANT: NEEVES, CHRISTOPHER D

APPLICANT: BEYEN

APPLICANT: BEYEN

TITLE OF INVENTION: BRYAN

TITLE OF INVENTION: BLOSYNTHETIC GENE CLUSTER FOR AMBRUTICINS

FILE REFERENCE: 010099.03

CURRENT APPLICATION NUMBER: PCT/USOS/07924

CURRENT FILING DATE: 2004-03-08

PRIOR APPLICATION NUMBER: US 60/551,103

PRIOR APPLICATION NUMBER: US 60/551,103

PRIOR PLING DATE: 2004-05-04

PRIOR FILING DATE: 2004-05-04
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Pred. No. 6.6;
0; Mismatches 74; Indels 3;
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FILE REFERENCE: 010099.03
CURRENT APPLICATION NUMBER: US/11/075,185
CURRENT FILING DATE: 2005-03-07
FRIOR APPLICATION NUMBER: US 60/551,103
FRIOR FILING DATE: 2004-03-08
FRIOR APPLICATION NUMBER: US 60/568,290
FRIOR FILING DATE: 2004-05-04
SOFTWARE: PALENT NOS: 61
SOFTWARE: PALENTIN VETRION 3.3
SEQ ID NO 35
FRIOR FILING DATE: 2004-05-04
SOFTWARE: PALENTIN VETRION 3.3
                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Sorangium cellulosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Sorangium cellulosum
PCT-USOS-07924-1
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1 Similarity 53.3%;
88; Conservative
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Matches 88; Conserv
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RESULT 9

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### AFPLICANT: HORELER, Heinz
| AFPLICANT: HORELER, Heinz
| TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell
| TITLE OF INVENTION: POOLIFERING: PROJECTION OF PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22099 GAGCACCTGCGCGCCCACCCGGACCAGCGGCTGCTCGACGTCGCCGCGGAGCCTGGCCACG
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Sequence 1, Application US/11075185
GREEAL INFORMATION:
APPLICANT: REID, RALPH
TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMBRUTICINS
TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR AMBRUTICINS
TILE REFERENCE: 010099.03
CURRENT APPLICATION NUMBER: US/11/075,185
CURRENT APPLICATION NUMBER: US 60/551,103
PRIOR APPLICATION NUMBER: US 60/551,103
PRIOR FILING DATE: 2004-03-08
PRIOR FILING DATE: 2004-03-08
PRIOR FILING DATE: 2004-03-08
PRIOR FILING DATE: 2004-05-04
NUMBER OF FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 61
SOFTWARE: Patentin version 3.3
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Pred. No. 7.7;
0; Mismatches
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GENERAL INFORMATION:
APPLICANT: FORENS, John
APPLICANT: HARBECK, Nadia
APPLICANT: KOENIG, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-11-075-185-1
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Best Local Similarity 53.3%;
Matches 88; Conservative
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MODEL, Fabian
NIMMRICH, Inko
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TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DROSOPHILA GENES.

FILE REFERENCE: CLOOO78

CURRENT APPLICATION NUMBER: US/11/097,143

CURRENT APPLICATION NUMBER: 60/157,832

PRIOR APPLICATION NUMBER: 60/160,191

PRIOR PLIING DATE: 1999-10-19

PRIOR APPLICATION NUMBER: 60/160,191

PRIOR APPLICATION NUMBER: 60/160,193

PRIOR PLIING DATE: 1999-11-12

PRIOR APPLICATION NUMBER: 60/133,383

PRIOR APPLICATION NUMBER: 60/173,383

PRIOR APPLICATION NUMBER: 60/173,383

PRIOR APPLICATION NUMBER: 60/173,383

PRIOR APPLICATION NUMBER: 60/194,831

PRIOR FILING DATE: 2000-02-24

PRIOR FILING DATE: 2000-03-23

NUMBER OF SEQ ID NOS: 43008

SOFTWARE: PASESEQ for Windows Version 4.0

SEQ ID NOS: 43008

TYPE: DAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45 GCCGGACGCAACTCCTTATCGGAACAGGACGCCCTCCATATCAGCCGCGCGTTATCTCA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    368 eccescratrecricarereresacesas acacerecarereres aces escential de la constante de la consta
                                                                                                                                                                                                                                                                                                               Sequence 2311, Application US/11031175
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Missen, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849) BL
CURRENT APPLICATION NUMBER: US/11/031,175
CURRENT FILING DATE: 2005-01-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 29.8; DB 11; Length 1311;
Pred. No. 9.7;
0; Mismatches 47; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105 TGCGCGTGACCGGACACGAGGCGCCCGTCCCGCTTATCGCGCCTTA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           428 GGAACGGGACATTGGACGGCCCGCCGGTCACGCTCTTTACCCCCCA 472
                                                                                           1465 CACTTCCTCCCAAPATCGCGCC 1444
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         126 CGCCCGTCCCGCTTATCGCGCC 147
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PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 2371
LENGTH: 1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 55.2%;
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
CRGANISM: Myxococcus xanthus
US-11-031-175-2371
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ORGANISM: DROSOPHILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-11-097-143-26108
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APPLICANT: MARA, ABMULL

APPLICANT: MEFER, Heinz

TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell

TITLE OF INVENTION: Detaile acids for the improved treatment of breast cell

TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell

TITLE OF INVENTION: DETAIL CAST 10.03

CURRENT APPLICATION NUMBER: US/10/517,441

CURRENT APPLICATION NUMBER: DE 10317955.0

PRIOR PILING DATE: 2003-04-17

PRIOR PELING DATE: 2003-04-17

PRIOR PELING DATE: 2003-01-07

PRIOR PELING DATE: 2003-10-01

NUMBER: DE 10245779.4

PRIOR FILING DATE: 2003-10-01

NUMBER OF SEQ ID NOS: 2147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1585 AACGCGAAACCACCGCTCCTCCTCCCAACGCCGCCGAAATAACCTCAACGCC 1526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 GAACAGGACGCCCTCCATATCAGCCGCGTTATCTCATGCGCGTGACCGGACACGAGG 125
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                                                                                                                                                                                                                                                                                                                                                                                                               6 ATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCG 65
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                      ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-517-441-401
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Pred. No. 9.1;
0; Mismatches 70; Indels
                                                                                                                                                                                                                        Query Match
16.9%; Score 30; DB 8; Length 3107;
Best Local Similarity 50.7%; Pred. No. 9;
Matches 72; Conservative 0; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1959 CACTTCCTCCCAATATCGCGCC 1938
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ORGANISM: Artificial Sequence
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16.9%;
Best Local Similarity 50.7%;
Matches 72; Conservative
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SCHMITT, Manfred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FOEKENS, John HARBECK, Nadia KOENIG, Thomas MAIER, Sabine MARTENS, John MODEL, Fabian NIWMRICH, Inko RUJAN, Tamas
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US-10-517-441-499/c
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Search completed: May 10
Job time : 437.346 secs
         JS-11-031-175-1101/c
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LENGTH: 13579
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                                                                                                                                                                                                                                                                                                                                                                                                                                             67 AACAGGACGCCCTCCATATCAGCCGCGTTATCTCATGCGCGTGACCGGACACAGAGGC 126
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                                                                                                                                                                                                                                                                      7 TCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: ARRAYS, FOR PIECTING EXPRESSION OF 10,000 OR MORE
FILE REFERENCE: CL000728
                                                                                                                                                                                   Gaps
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                                                                                            Length 1789;
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                                                                                       16.8%; Score 29.8; DB 10; 49.1%; Pred. No. 9.9;
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Best Local Similarity 49.1%; Pred. No. 11;
Matches 79; Conservative 0; Mismatches 82;
                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR PLILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-19
PRIOR PILING DATE: 1999-10-19
PRIOR PILING DATE: 1999-10-19
PRIOR PELING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/161, 932
PRIOR APPLICATION NUMBER: 60/164, 769
PRIOR PLILING DATE: 1999-11-12
PRIOR PLILING DATE: 1999-11-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 26107, Application US/11097143
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/184,831
FILING DATE: 2000-02-24
APPLICATION NUMBER: 60/191,637
FILING DATE: 2000-03-23
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                                                                                                                                                                               Conservative
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US-11-097-143-26107
                                                                                                                            Best Local Similarity
Matches 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-11-097-143-26107/c
US-11-097-143-26108
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LENGTH: 3915
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RESULT 15

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## Sequence 1101, Application US/11031175

| Sequence 1101, Application US/11031175
| APPLICANT: Goldman, Barry S.
| APPLICANT: Goldman, Barry S.
| APPLICANT: Hinkle, Gregory J.
| TILE OF INVENTION: Wycoccus xanthus S.
| CURRENT APPLICATION NUMBER: 60/217, 883
| PRIOR PPLICATION NUMBER: 60/217, 883
| PRIOR PRILING DATE: 2005-0-1-08
| PRIOR PLING DATE: 2005-0-1-08
| PRIOR PRILING DATE: 2005-0-1-08
| PRIOR PLING DATE: 2005-0-1-08
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UI-CF-DU1

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 50; Mallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="CIT Approved Human Genomic Sperm Library D" /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
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sapiens genomic clone Plate=2266 Col=15 Row=A, genomic survey
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
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Pred. No. 5.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
|mol_type="genomic DNA"
| Ab_xref="txxon:5606"
| Ab_ore="Plate=2266 Col=15 Row=A"
                                                                                                                                                                                                                                                                                                  ALIGNMENTS
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Fax: (206) 616-3887
Email: jwallace@u.washington.edu
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            GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
                                                                                                                                      106 TTTCTTTAGTGCACCCTACCATCCTGTGGCATGAGAATCCGCTATCACCCCCTTATG 165
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                                                                                                                                                                                                                                                          166 GGCACAGCCCTTCCAACCAGCTCGTGCCCAGAGAACACATGACCGGCATTTCAACCAAT
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prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST 06-DEC-2002
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissues were provided by Vassilis Aidinis ( Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari, Greece ) whose assistance we gratefully acknowledge.
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                                      Compared with
Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
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/clone_lib="RIKEN full-length enriched, whole joints"
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Pred. No. 5.9;
0; Mismatches
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Best Local Similarity 51.7%;
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Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Marthonni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Paran, W.J., Pertea, G., Pesole, G., Percovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takeraka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlested, C., Wanngy, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wannes, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Komo, H., Nakamura, M., Sako, K., Shiraki, T., Kawai, J., Aizawa, K., Sakasume, N., Hirozane-Kishikawa, T., Kawai, J., Aizawa, K., Sakasume, N., Kagwa, I., Miyazaki, T., Waterston, R., Lander, E.S., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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Email: genome-res@gc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozanie,T., Imotani,K., 18hii,Y., Toh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,N., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission Compuse cDNAs Compared with
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
Genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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/clone="K630011C08"
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Fax: 81-45-503-9216
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CV068875 931 bp mRNA linear EST 24-AUG-2004 f2 new chopped.fasta.Contig488 Preamplified custom cDNA library in pCMV8port6.1 (ResGen, Invitrogen Inc.) Emiliania huxleyi cDNA, mRNA
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Eukaryota, Haptophyceae; Isochrysidales; Emiliania.
I (bases 1 to 91).
Wahlund,T.W., Zhang,X. and Read,B.A.
Expressed Sequence Tag Profiles from Calcifying and Non-Calcifying
149 CCTCACCAGCTCGCACTCTCCTCGGGGGCGCACGGCTCGCCGTGCCCCTGCCCACCANGG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             425 ACCTGCTCCGGCCGCCGCGGTCTCGCAACAGGCCGAGTCCGCGCAACAGTCGCCCGAG 484
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 348)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="Late_log growth phase"
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(Guillard's F/2 media)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39 ACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGCGCCTCCATATCAGCCGCGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Department of Biological Sciences
California State University San Marcos
333 S. Twin Oaks Valley Road, San Marcos, CA 92096-0001, USA
Tel: 760 750 4129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Emiliania huxleyi"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cultures of Emiliania huxleyi
Micropaleontology (2004) In press
                                                 123 AGGCGCCCGTCCCGCTTATCGCGCC 147
                                                                                             209 GACAGAGCGTCCCGCTTCCC 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bread@csusm.edu.
Location/Qualifiers
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/strain="1516"
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19.0%; Score 33.6; DB 5; Length 402; 51.7%; Pred. No. 5.9; ive 0; Mismatches 70; Indels

75; Conservative

Best Local Similarity

Matches

Query Match

62

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Nikaido, I., Osato, N., Sasukawa, T., Adachi, J., Bono, H., Kondo, S., Kiyosawa, H., Yagui, K., Tomaru, Y., Hasegawa, Y., Nogami, J., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, M., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Belsel, K.W., Blake, J.A., Frazer, K.S., Gaasterland, T., Goribbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gassi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kawaji, H., Kawasawa, Y., Lee, Y., Lenhard, B., Lyons, P.H., Maglott, D.B., Maltais, L., Marchionni, L., WcKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, K., Pontius, J.U., Qi, D., Ramachandran, S., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, B.D., Tomita, M., Verardo, R., Wanger, L., Wahlestedt, C., Wanagisawa, M., Yang, I., Wanger, L., Wahlestedt, C., Wanagisawa, M., Yang, I., Yang, L., Wanger, I., Wahlestedt, C., Wanagisawa, M., Yasuninci, P., Hayateu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sato, K., Shirak, Y., Kana, J., Aizawa, K., Shirak, Y., Kawai, J., Aizawa, K., Shirak, J., Yashino, M., Waterston, R., Lander, E. S., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length conse
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1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216

Fax: 81-45-503-9216

Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozande-T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Shiraki,T., Tagami,M., Nakamura,M., Nomura,K., Sato,K., Shibata,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Namm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected CDNAs to
prepare full-length cDNA libraries for rapid discovery of new
Genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence of in Mouse Genome
CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Davision of Experimental Animal Research in Riken contributed to
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Tissues were provided by Vassilis Aidinis ( Biomedical Sciences
Research Center 'Al. Fleming' Institute of Immunology 14-16 Al.
Fleming street 16672 Vari, Greece ) whose assistance we gratefully
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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/db xref="taxon:10090"
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COMMENT

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Mammalia butnerla; Kodentia; Scillrognath; Muridae; Murinae; Murin
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                               /tissue type="whole joints"
/clone_lib="RIKEN full-length enriched, whole joints"
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                                                                                                                                                                                18.6%; Score 33; DB: 51.7%; Pred. No. 9.2; tive 0; Mismatches
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/clone="L230014G21"
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Mus musculus
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                                                                                                                                                                                                                                                              75; Conservative
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Best Local Similarity
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BY337247
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Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Bisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, B., Dragani, T.A., Fletcher, C.F., Forzes, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godik, A., Gough, J., Grimmond, S., Gariboldi, M., Gissi, C., Godik, A., Gough, J., Jarvis, E.D., Kanai, A., Kawali, H., Kawasawa, N., Jackson, I.J., Jarvis, E.D., Konagaya, R., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Mixi, H., Nagashima, T., Numata, K., Okido, T., Portius, J.U., Reid, J., Ringy, B.Z., Kingwald, M., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Ringy, B.Z., Kingwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sultana, R., Yakenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Walls, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yang, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Komno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Alazwa, K., Arakawa, T., Fukuda, S., Hara, H., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Rogers, J., Birney, B., and Hayashizaki, Y., Raswa, T., Pukuda, S., and Hayashizaki, Y., Raswa, T., Pukuda, S., and Hayashizaki, Y., Sasaki, D., Shirasy, P., Shirashi, A., Yoshino, W., Waterston, R., Lander, E.S., Rogers, J., Birney, B., and Hayashizaki, Y., Sasaki, D., Shirasy, P., S
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Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozand.K., Imbiai,Y., Tohii,Y., Tohi,W., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
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Computational Analysis of Full-Length Mouse cDNAs Compared with
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Normalization and subtraction of cap-trapper-selected cDNAs to
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10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia real-time sequence Caboration of a
nonredundant cDNA library. Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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/cell_line="RCB-0558 LLC"
/clone_lib="RIKEN full-length enriched, lung RCB-0558 LLC
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Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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/db_xref="taxon:10090"
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Fax: 81-45-503-9216
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                                            Email: genome-resegnc.riken.jp, URL:http://genome.gsc.riken.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozani,K., Ishii,Y., Itahii,Y., Tuch,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazune,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subrraction of cap-trapper selected cDNAs to
prepare full-length cDNA libraries for rapper selected cDNAs to
prepare full-length cDNA libraries for rapper selected cDNAs to
prepare full-length cDNA libraries for rapper selected cDNAs to
prepare full-length cDNA libraries for rapper selected cDNAs to
prepare decome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia real-time sequence clustering for construction of a
nonredundant cDNA library Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues
riseuss were provided by Vassilis Aidnis ( Biomedical Sciences
Research Center 'Al. Fleming' Institute of Immunology 14-16 Al.
Pleming street 16672 Vari, Greece ) whose assistance we gratefully
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BY013584 BXTEM full-length enriched, lung RCB-0558 LLC cDNA Mus musculus cDNA clone G730040E06 5', mRNA sequence.
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Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikaido,I., Osato,N., Saito,K., Suzuki,H., Yamanaka,I.,
Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A.,
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/clone_lib="RIKEN full-length enriched, whole joints"
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Pred. No. 9.2;
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/clone="L230006D15"
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Matches 75; Conservative (
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FEATURES

DRIGIN

셤 ઠે 셤 ò KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

DEFINITION ACCESSION VERSION

RESULT 7 BY013584

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Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (Razaki,Y.; Furuno,M.; Kasukawa,T.; Adachi,J.; Bono,H.; Kondo,S.; Kiyosawa,H.; Yagi,K.; Tomaru,Y.; Hasegawa,Y.; Nogami,A.; Kiyosawa,H.; Yagi,K.; Tomaru,Y.; Hasegawa,Y.; Nogami,A.; Schonbach,C.; Gojobori,T.; Baldarelli,R.; Hill,D.P.; Bult,C.; Hume,D.A.; Quackenbush,J.; Schriml,L.M.; Kanapin,A.; Matsuda,H.; Retcher,C.; Gojobori,L.B.; Cousins, S.; Dalla,B.; Dragani,T.A.; Fletcher,C.F.; Forrest,A.; Frazer,K.S.; Gaasterland,T.; Gariboldi,M.; Gissi,C.; Godzik,A.; Gough,J.; Gariboldi,M.; Gissi,C.; Godzik,A.; Gough,J.; Gariboldi,M.; Gissi,C.; Godzik,A.; Gough,J.; Garriboldi,M.; Gissi,C.; Godzik,A.; Gough,J.; Garvis,B.D.; Kanaji,H.; Kawasawa,Y.; Kedzierski,R.M.; King,B.L.; Konagaya,A.; Kavaji,H.; Kawasawa,Y.; Lenhard,B.; Loons,P.P.; Maltais,D.; Marchionni,L.; Marchion,R.; Sendelin,A.; Schneider,C.; Semple,C.A.; Setou,M.; Shimada,K.; Sandelin,A.; Schneider,C.; Semple,C.A.; Setou,M.; Sandalama,R.; Takenaka,Y.; Taylor,M.; Tasadale,R.D.; Tomita,M.; Verardo,R.; Walming,L.G.; Wynshaw-Boris,A.; Yanagisawa,M.; Yangi,T.; Walsteu,N.; Hirozane-Kishikawa,T.; Wangi,Y.; Marchion,H.; Marchion,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BY340467 RIKEN full-length enriched, whole joints Mus musculus cDNA BY340467.

BY340467 ST 12-DEC-2002
BY340467
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho,
Tel: 81-45-503-922
Fax: 81-45-503-9216
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Alazwa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Almurai,K., Ishii, Y., Itoh,W., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
                                                                                                                                                     3 CTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTA
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               DB 5; Length 354;
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                                          Pred. No. 9.2;
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           Score 33;
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Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
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Okazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyoswa, H., Yaqi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Pletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tissues were provided by Vassilis Aidinis (Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari, Greece ) whose assistance we gratefully
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
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Pred. No. 9.2;
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/clone="L230028H13"
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362 bp mRNA linear EST 12-DEC-2002 BY339252 RIKEN full-length enriched, whole joints Mus musculus cDNA clone L230021B07 5', mRNA sequence.
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Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Kanai, A., Kawai, H., Kawasawa, Y., Jackson, I.J., Jarvis, B.D., Kanai, A., Kawai, H., Kawasawa, Y., Kedzierski, R.M., King B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lehard, B.L., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Parvan, W.J., Pertea, G., Pearochandran, S., Petrovsky, N., Pillai, R., Pontius, Ju., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shinada, K., Sultana, R., Takenaka, Y., Taylor, M. S., Teasdale, R. D., Tomita, M., Verardo, R., Wanner, L., Wahleetedt, C., Wang, Y., Watcanabe, Y., Wallming, L.G., Wynshaw-Boris, A., Yang, I., Yang, I., Yang, I., Yang, I., Yang, I., Yang, I., Xaro, M., Milming, L.G., Mynshaw-Boris, A., Yang, I., Alzawa, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Alzawa, T., Rukda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Myyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length, Cana
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Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
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Tissues were provided by Vassilis Aidinis (Biomedical Sciences Tissues were provided by Vassilis Aidinis (Biomonology 14-16 Al. Fleming street 16672 Vari, Greece ) whose assistance we gratefully acknowledge.
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/tissue_type="whole joints"
/clone_lib="RIKEN full-length enriched, whole joints"
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/db xref="taxon:10090"
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Mammalia, Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mukmalia; Eutheria; Rodentia; Sciurognath; Muridae; Murinae; Mukmalia; Eutheria; Rodentia; Sciucki, Y., Rosuka, Y., Nogami, A., Saito, R., Suzuki, H., Yanganaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Corbani, L.B., Cousina, S., Dalla, B., Dragani, T.A., Batalov, S., Beisel, K.W., Elaket, J.A., Bradt, D., Brusic, V., Chothia, C., Corbani, L.B., Cousina, S., Dalla, B., Dragani, T.A., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., L., Miki, H., Nagashima, T., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pertea, G., Pertea, G., Pesolo, G., Readio, T., Red, J., Ring, B. Z., Ringwald, M., Sultana, R., Takenaka, Y., Taylor, M.S., Tagaslima, T., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Waranabe, Y., Verardo, R., Wanger, L., Wahlestedt, C., Wang, Y., Waranabe, Y., Wang, L., Wahlestedt, C., Wang, Y., Waranabe, Y., Wang, L., Yang, L., Yang, L., Wahlestedt, C., Wang, Y., Waranabe, Y., Garninci, P., Hayateu, N., Hirozane Kishikawa, T., Yang, Y., Zayon, H., Nakamura, M., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Shiraki, A., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, B. and Hayashizaki, Y., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
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1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
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Hayashizaki,Y. Direct Submission
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Gaps ;

18.6%; Score 33; DB 5; Length 360; nilarity 51.7%; Pred. No. 9.2; Conservative 0; Mismatches 70; Indels

Best Local Similarity Matches 75; Conserva

Query Match

FEATURES

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Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S.,
Rogers,J., Birney,E. and Hayashizaki,Y.
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Hirozane,T., Imotani,K., Ishhi,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Shiraki,T., Tagani,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequence din Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-ho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
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/dev_stage="10 days neonate"
/clone_lib="RIKEN full-length enriched, 10 days neonate
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Yoshihide Hayashizaki
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/strain="C57BL/6J"
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                                                                                                                                                                                                                          sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Science Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fishes were provided by Vassilis Aidinis (Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari, Greece ) whose assistance we gratefully
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 371)
Okazaki, Y., Puruno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaldo, I., Osato, N., Saito, R., Yananaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hame, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blaes, Bradt, D., Brusic, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustinoich, S., Hirokawa, N., Jackson, I.J., Jarvis, B.D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length CDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence, analysis (RRSA) system-384-format
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/tissue_type="whole joints"
/clone_lib="RIKEN full-length enriched, whole joints"
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/db_xref="taxon:10090"
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Best Local Similarity
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VERSION
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BY083658
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/clone lib="Talri"
/note="Vector: Lambda ZaplI; mass excised in plasmid
/note="Vector: Lambda ZaplI; mass excised in plasmid
vector pBK-CMV (Stratagene). Site 1: ECORI; Site 2: XhoI;
mRNA obtained from wheat NIL Thatcher Lr1 24 hours after
inoculation with leaf rust pathogen Puccinia triticina
race BBB carrying the avirulence gene Avrl."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BQ620008 621 bp mRNA linear EST 28-JUN-2002
TaLr1138G03F TaLr1 Triticum aestivum cDNA clone TaLr1138G03F, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sukaryotta, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Tritice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: (204) 983-2340

Fax: (204) 983-4604

Bmail: scloutier@arg.c.ca

primer where from the 5' end (same with forward primer and 3'end).

Average insert size is >2.2kb

Plate: 138 row: G column: 03

Seq primer: M13 Forward.
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                                                                                                  18.6%; Score 33; DB 7; Length 611; 51.7%; Pred. No. 9.3; 1.1%; Pred. 0; Mismatches 70; Indels
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Best Local Similarity 51.7%; Pred. No. 9.3;
Matches 75; Conservative 0; Mismatches 70; Indels
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/mol type="mRNA"
/cultivar="Thatcher Lr1"
constructed by Yulan Piao."
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/tissue_type="Leaf tissue"
/dev_stage="14 Days old"
/lab_host="E. coli XLOLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               CF916169 h. A. A. CF-NOV-2003 611 bp mRNA linear EST 05-NOV-2003 B0991A12-5 NIA Mouse Unfertilized Egg cDNA Library (Long 1) Mus musculus cDNA clone NIA:B0991A12 IMAGE:30480971 5', mRNA sequence.
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Piac,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.
CONStruction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
                               TCGGAACAGGACGCCCTCCATATCAGCCGCGCTTATCTCCATGCCGCGTGACCGGACACG 122
                                                                                                     171 CCTCACCAGCTCGCACTCTCCTCGGGGGGCACGGCTCGCCGTGCCCTGCCCAGCACGG 230
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
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/mol_type="mtNA"
/strain="C57BL/64"
/db_xref="nia8ST:80991A12-5"
/db_xref="taxon:10090"
/clone="NA:80991A12 IMAGE:30480971"
/dev stage="Unfertilized Egg"
/lab_host="DH108"
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Plate: B0991 row: A column: 12
Seg primer: M13 Reverse
High quality sequence stop: 611
POLYA=No.
                                                                                                                                                                            123 AGGCGCCCGTCCCCCTTATCGCGCC 147
                                                                                                                                                                                                                                                      231 GACAGAGCGTCCCGCTTCCCTCTCC 255
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COMMENT
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/clone lib="Sugano mouse kidney mkia"
/clone lib="Sugano mouse kidney mkia"
/note="Organ: kidney; Vector: pME186-FL3; Site 1: DraIII
(CACTGTGTG); Site 2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCTTTTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [GTTGGCCACTGG], digested
and cloned into distinct DraIII sites of the pWE188-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AW319335 635 bp mRNA linear EST 25-JAN-2000 unl1f04.yl Sugano mouse kidney mkia Mus musculus cDNA clone IMAGE:2395039 5' similar to TR:Q9YGP5 Q9YGP5 RRM-TYPE RNA-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                63 TCGGAACAGGACCCCCCCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACACG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            152
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Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Onderwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pepc,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., The WashU-NCI Mouse EST Project 1999
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This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                        3 CTTATCGTGACAGGACGCCAGCTTCCTGTGGTAACCGCAGCCGGACGCAACTCCTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 cércaccadorcida de references de deserces de confecciones d
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
TTE1: 314 286 1800
Fax: 314 286 1810
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0
                                                                                                                            Length 624;
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                                                                                                                    DB 7;
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constructed by Yulan Piao."
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                                                                                                                        Score 33;
Pred. No.
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High quality sequence stop: 305.
Location/Qualifiers
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/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:2395039"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 AGGCGCCCGTCCCCCTTATCGCGCC 147
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/lab_host="DH10B"
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Mus musculus
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51.7%;
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                                                                                                                                                                                                75; Conservative
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Matches 75: Conserv
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 6.24)
Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S. H.
Construction of long-transcript enriched cDNA libraries from
submicrogram amounts of total RNAs by a universal PCR amplification
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                                81 CCATATCAGCCGCGTTATCTCATGCGCGTGACCGGACACGAGGCGCCCGTCCCGCTTA 140
                                                                                                        clone_lib="NIA Mouse Unfertilized Egg cDNA Library (Long
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National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
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dev stage="Unfertilized Egg"
lab_host="DH10B"
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Plate: B0950 row: D column: 02
Seg primer: M13 Reverse
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/mol_type="mRNA"
/strain="C57BL/6J"
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                                                                                                                                                                                                                                                            555 CGGCACGAGGCGCACACAAGCCAA 579
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Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end
primer CGACCTGCAGCTCGAGCACA."
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Search completed: May 10, 2005, 07:25:12 Job time : 1244.12 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

Run on:

May 10, 2005, 03:40:34; Search time 3416.8 Seconds (without alignments) 7998.346 Million cell updates/sec

US-09-896-888A-1 564

Perfect score: Sequence:

1 catgatgataaacaatgtat.........tgttacagcgacacaacatg 564

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4708233 segs, 24227607955 residues Searched:

Total number of hits satisfying chosen parameters:

9416466

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl:\* Database :

90 ba: \*
90 htg: \*
90 par: \*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

					SUMMARIES	
Result		Query	•	;	;	
No.	Score	Match	Match Length DB	BB	ID	Description
н	564	100.0	564	9	BD070856	BD070856 Insect ex
7	564	100.0	4170	14	NPHTTAA	M83827 Orqyia pseu
m	564	100.0	131995	14	OPU75930	U75930 Orgyia pseu
O 4	562.4	99.7	1429	14	864501	S64501 p8.9=8.9 kd
S	548	97.2	2773	9	AX766573	AX766573 Sequence
9 0	111.8	19.8	118584	14	AY043265	AY043265 Epiphyas
7	101.8	18.0	131526	14	AY145471	AY145471 Rachiplus
ص ت	101.4	18.0	18.0 1511	14	NPHPE38	M62488 Autographa
o 0	101.4	18.0	133894	9	A48542	A48542 Sequence 1
c 10	101.4	18.0	133894	14	L22858	L22858 Autographa
11	100	17.7	131158	14	AY327402	AY327402 Choriston
c 15	93.4	16.6	28413	9	BD187790	BD187790 A virus i
c 13	93.4	16.6	128413	14	NPHT3COMP	L33180 Bombyx mori
c 14	92.2	16.3	129609	14	AF512031	AF512031 Choriston
c 12	92	16.3	2178	14	NPBBMIEN	D14467 Bombyx mori
16	90.4	16.0	16.0 2011	14	NPHIEN	M59422 Autographa
17	73.8	13.1	155060	14	MBU59461	U59461 Mamestra co
18	72.2	12.8	4051	14	AF246708	AF246708 Spodopter
9	72.2	12.8	139342	14	AP125155	AF325155 Spodopter

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Gaps

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Length 564; 0; Indels

Query Match
100.0%; Score 564; DB 6;
Best Local Similarity 100.0%; Pred. No. 4e-171;
Matches 564; Conservative 0; Mismatches 0;

1. .564
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/mol\_type="genomic DNA"
/db\_xref="taxon:32644"

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AF539999 Mamestra	Mamestra	AF303045 Helicover	Q)	AF334030 Helicover			APU062/0 Adoxopnye av327402 Choriston	. თ				CR376837 Danio rer Exchoses Zebrafieb	AX599005 Sequence					AC093559 Homo sapi	ACT23846 MIS MISCOLI	CO.		DNA linear PAT 27-AUG-2002					, Pfeifer,T.A. and Hegedus,D.D.	25.28B-2001.	12021, 31A	ovirus			60/049946, 28-JAN-1998 CA 2221819 PI	THEILMANN, THOMAS		59//C12N9/22		lalitiers	/organism='Multicapsid nucleopolyhedrovirus'.	,	
AF539999	AY126275	AF303045	HZU67264	AF334030	AF271059	AF081810	AF006270 AY327402	AC151093	AX598859	AX251255	AX767469	CR376837	AX599005	AX767545	AC150919	AC020384	AL449063	AC093559	AC123846	AR424142		564 bp		159			Theilmann, D.A.,	œ -	TISH COLUMBIA	eopolyhedro	1	1998541010	60/049946	DAVE A THEII		06,C12N15/	expression vectors	Location/Un	/ordanism='	lifiers	
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SAPRAAPRRVHAVGDPGAPLRASYALPNGVYNLHGDAHFNPPEEDDDILFVDTAAEQA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTG
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                                                                                                                                                      /codon_start=1
/product="transcriptional trans-activator"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 564; DB 14;
100.0%; Pred. No. 6.1e-171;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="ORF; homologous to
/codon start=1
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/db_xref="G1:332542"
                                                                         657. .>1908
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691. .1908
                                                                                                                                                                                                                                                                                                                                                                                 1958..1963
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2915..2922
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The limani, D.A. and Stewart, S.
Tandemly repeated sequence at the 3' end of the IB-2 gene of the baculovirus Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus is an enhancer element
Virology 187 (1), 97-106 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Orgyia pseudotsugata nuclear polyhedrosis virus transcriptional trans-activator (IE-2) gene, complete cds; ORF, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source text: Orgyia pseudotsugata nuclear polyhedrosis
                                         TTTTCATGTTTGCCAACAACACCCTTTATACTCGGTGGCCTCCCCACCACCAACTTTTTT
                                                                                                                  GTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACACTACCACAC
                                                                                                                                                                                               GTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACACTACCACAC
                                                                                                                                                                                                                                                   ATTGAACCTTTTTGCAGTGCAAAAAGTACGTGTCGGCAGTCACGTAGGCCCGGCCTTATC
                                                                                                                                                                                                                                                                        GGGTCGCGTCCTGTCACGTACGAATCACATTATCGGACCGGACGAGTGTTGTCTTATCGT
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Orgyia pseudotsugata single capsid nuclopolyhedrovirus
Orgyia pseudotsugata single capsid nuclopolyhedrovirus
Orgyia pseudotsugata single capsid nuclopolyhedrovirus
Viruses, dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.

1 (bases 1 to 4170)

Theilmann, D.A. and Stewart, S.

Molecular analysis of the trans-activating IE-2 gene of seudotsugata multicapsid nuclear polyhedrosis virus
Virology 187 (1), 84-96 (1992)

    4170
    /organism="Orgyia pseudotsugata single capsid
nuclopolyhedrovirus"
muclopolyhedrovirus"
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MRRRQCYNDPAALKNVRNLMARDFVFCLTRFNFECRSTDYKQIAKHSFLASRHDYI" 946. 2370 /note="ORE2; similar to AcMNPV ORF9" /note="ORE2; similar to AcMNPV ORF9" /codon start=1 /product="1629-capsid" /protein id="Ac59001.1" /db xref="161:2934904" /translation="WMERQYSURSYLINNQHNAIAAGPFLQRVAGPEAHSVGRNVGD /translation="WMERQYSURSYLINNQHNAIAAGPFLQRVAGPEAHSVGRNVGD RAYRLNRQAYLDLLALAEDIYADTAYMQADQPEASSRHFATLNRNRLLLIGVQDPDAR RANASVLARIEALISVDVNDAEVNVLSGDFYESTSKISYQTFRQTPTASASQOTO TSLPRPQTSLPRQTQASLPQQTPFDQPEMVSPPSFVHTTPAILPQTTQPPATDTFSRP SDEFYTYPGKERAVPDTRFRPPPPREHLKSRRSSVATNAAGARPVARPPPPFFSAD VTTSMPPPPFPSADVTTSMPPPPREHLKSRRSSVATNAAGARPVARPPPPFFSAD INNLLIDAMVAETINNAGDNRSALLDQIKQGTLLKTQPADGARATDPRSTLLSSIRQ GKTLKKLRKEBQSSTQTLLKQUYTDKTKTILKUFVTNIDRISKQGGERKORLDTT	KRRPAVEHTDGNSTGNNSDDWRDD"  complement (15333270)  /note="URF8"; ph; similar to AcMNPV ORF8"  /codon_start=1 /product="Polyhedrin"  /protin_id="AAC59002.1" /brotin_id="AAC59002.1" /db_xref="Gf1:1911249" /translation="WPDYSYRPTIGHTYVYDNKYYKNIGSVIKNAKRKKHLLEHEEDE KHIDELDHYMVAEDPFLGFRANGKLITHERINVKPDTWKLITNWSGKEFLRETWTRF VEDSFPINYDGWANDTFLVYNARPTRENKCYKFLAGHALWDCDYVPHEVIR IVENSY VGMNNEYRISLAKKGGGCPIMNIHAEYTNSFESFVNRVIWENFYKPIVYIGTDSSEEE EILIEVSLVPKVKERAPDAPLETGRAY"  complement (33503541) /note="ORF4"	/codon_grart=1 /product="unknown" /protein_id="AAC59003.1" /db_xref="GI:1911250".1" /db_xref="GI:1911250".1" /db_xref="GI:1911250".1" /db_xref="GI:1911250".1" /db_xref="GI:1911250".1" /codo="CREW /codon_grart=1 /codon_grart=1 /product="unknown" /protein_id="AAC59004.1" /db_xref="GI:1911251" /trainslation="MASSONGRILKLFYRWSSOTGAALDDEKDLHCLYDLERFVGA	HINKRADDKARKKKCAEKAALKRUEIAADRHMIERAAAPRCADDGRWSTLSRAQLDDI ARBERIVDR.HRLOLKODSLIKQDRLKKR" complement (4125. 4739) /note="norts" 16f-2; similar to AcMNPV ORF6" /codon_start=1 /product="late expression factor 2" /protein_id="AAC59005.1" /db_xref="not-"MERVWNRARGIOGLKRSETYLVDPHDFVGVLTLSPYTVFERGLFVRDSTORTOLICALIAAPRYQEPOPAVRRPPGRSRRNYCLKACADGAQSLAKVIAARVSMPPCMSTHALIAAPRYQEPOPAVRRPPGRSRRNYCLKACADGAQSLAKVIAARVSMPPCMSTHALIKAQDVYKESNCAKMKKYTKLCPQASMCKGLNPICNF" /complement (4742. 4975)	/ Godon_State=] / codon_state=] / product="unknown" / product="unknown" / product="unknown" / procein_id="AAC59006.1" / db_xref="fd1:1911253" / translation="MNRPTMRNTAAVTTDYDREQLRRELNSLRRSVHELCTRSATGFD CNRFLEAGDRAPAVIYKAAANGGQHSSLICDKV" 5020. 5460 / note="0RF8; similar to AcMNPV ORF4" / codon_state=] / product="unknown" / product="unknown" / protein_id="AAC59007.1" / db_xref="fd1:1911254" / translation="MPGARFYRPSLRLTQBFKENVVAHVDHLMGLRALIDGKVTSADV RRFGFLSRNYLVSACMANNVQYAPDATIDMRHQPTIYRRVCQNCHAMADVBADDHS IARYLLABCGAVLVIDHPLDVFGETEGGVNELLEVQRINAGGDL" / note="ORF9; ptp-2" / note="ORF9; ptp-2"
CDS	SO SO	SQD	CDS CDS	CD CDS
	PRESULT 3 OPU75930 LOCUS LOCUS LOCUS OPU75930 LOCUS LOCUS DEFINITION Orgyia pseudotsugata multicapsid nucleopolyhedrovirus, complete accession U75930.2 GI:11024985 VERSION U75930.2 GI:11024985 SOURCE ORGANISM Orgyia pseudotsugata multicapsid nucleopolyhedrovirus ORGANISM Orgyia pseudotsugata multicapsid nucleopolyhedrovirus VITUSES; GDNA viruses, no RNA stage; Baculoviridae; Nucleopolyhedrovirus Uiruses, Lo 131995)	Ahr Roh The Pol Vir 912 912 2 2 801 Roh Dir Sub		SOUTCE 1119199    Aucleopolyhedrovirus"

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                                                                                              CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTG
                                                                                                                                                                                          TTTTCATGTTTGCCAACAAGCACCTTTATACTCGGTGGCCTCCCCACCACCAACTTTTTT
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  ; Score 564; DB 14;
; Pred. No. 1.3e-170;
0; Mismatches 0;
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                                                                                         /translation="MYEASQIDEHVFVGGYYGDNEAMLRFIENHAIASVISLIDSDVA
PIRHALGLPVGDHIHVYCEAAPTCAALPNAMPALYDYMVRRIGEGKRVLVHCYAGASR
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/tamalat.or="dd::1911257"
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VYGRFCALGREHFAHHKTACMHILFQFMRNDLTPADBERHPCFGVIKDFGRQCKDTYTA
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AQCFAYIVRNSISDYHVWPLEEGGREWYIDADPROCADVEALMLKVNVGATAFWLFF
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SFADCVRRAVHMYIGDAREDLVLRYWPDVDRDVFCNANKQIRAPFSYNYKGGDIRPG
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VALPRNVLAOKWFSQTAVLRHKNVVAFVTQAGLOSSDEALQARVPMVCLPMMGDOFHH
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HWTHGLNRSGYLVCRYMVERLGVSPTDAIARFETARGHKIERTNYLQDLLARKHVRGQ
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TADNYMGLIEMFKDQPDNANVRRFLSTNRTFDAVVVEAFADYALVFGHLFRPAPVIQI
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KQQFGKSTPTIRQLRDNVQLLLLINLHPVYDNNRPVPPSVQYLGGGLHLAQALPQRLDA
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                                                                                                                                                                              complement(6129. .6791)
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protein id="AAC59009.1"
db xref="GI:1911256"
                        tyrosine phosphatase 2"
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/note="ORF12; similar to AcMNPV ORF13"
/codon_start=1
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/note="ORF11; similar to AcMNPV ORF11"
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db_xref="G1:1911259"
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                                           protein_id="AAC59008.1"
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S64501 1429 bp DNA linear VRL 30-SEP-1993 p8.9=8.9 kda basic protein [Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus OpMNPV, Genomic, 1429 nt].
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1 (bases 1 to 1429)

Nu.X., Stewart,S. and Theilmann,D.A.

Characterization of an early gene coding for a highly basic 8.9K protein from the Orgyia pseudotsugata multicapsid nuclear
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nucleopolyhedrovirus"
/mol type="genomic DNA"
/db_xref="taxon:164623"
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128712 CATCTGTTACAGCGACACACATG 128735
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; Bratt, Tomas (DK) ; Voldborg, Bjorn (DK) ; Mouritsen, Soren
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                                                                                                            'note="p220p2F expression vector for insect cells"
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100.0%; Pred. No. 8.6e-166;
ive 0; Mismatches 0;
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                                                                                                                          561. .566
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                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Aval site"
2294. .2299
/note="Aval, Smal, a
2551. .2556
/note="Apall site"
                                 Location/Qualifiers
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/note="Aval site"
586. .591
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                                                                                                                                                                                                                                                     525. .630
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                                                                                                                                                                                                                                                                                                                                                                  note="PstI site"
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Best Local Similarity 100.
Matches 548; Conservative
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                                                                                                           /protein_id="AAB27738.1"
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Patent: WO 03042244 60 22-MAY-2003;
Pharmexa A/S (DK) ; Klysner, Steen (DK) ; Nielsen, Finn Stausholm
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                                                                                                                                                                                                       99.7%; Score 562.4; DB 14; Length 1429; 99.8%; Pred. No. 1.6e-170; ive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                          763. .990
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/note="8.9 kda basic protein"
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Sequence 60 from Patent WO03042244.
AX766573.1 GI:32260450
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VERSION
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SOURCE
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TITLE
JOURNAL
    gene
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complement (2717. .3070)
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                                                                                                                                                                                                                                                                                                                                                                                                     complement (2104. .2715)
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complement (1713. .2090)
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                                                                         codon start=1
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                                                                                                                                                                                                                                                                                                                                                                      /gene="lef-2"
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/note="ORF6"
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/note="ORF8"
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                                                                                                                                                                                                                                                                          Epiphyas postvittana nucleopolyhedrovirus, complete genome.
AY043265
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LANIVSRVEHLLRYEIVNDVBITTLSGDFYBEYSKYAARQYALSIQMPPPPPVITPLP
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/tc_xref="G1:1521312
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LPVTPTKPLIPLPKPBHLKFKRTITISBLPDMMATNNIDDQGATAPAPPPPPPPTBFBPFL
PSNDLPPPPPPPLTSGNVPPPPPTEGMLDDMLINAITAGNNKSEKNYTDARGDMLIN
IKKGVTLKPSKTINKSDKKVDDRADLLNSIKIGVKLKPIKVNINQPLPBAPVTDISVIA
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RTNSELPKLLDNVFSLLDRKPRSVENVNEAKNILDNLKERVKLTSNQLDNAEAQSLYI
NDPNQFYIQVEDLIFAGRYADAKMHLDLAITESGNDERLRRLKKFANDLDAVVV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (03-JUL-2001) Microbiology, University of Otago, PO Box
56, Dunedin, New Zealand
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Epiphyas postvittana nucleopolyhedrovirus postvittana nucleopolyhedrovirus bostvittana nucleopolyhedrovirus Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Nucleopolyhedrovirus.

1 (bases 1 to 116584)

Hyink, O., Dellow, R.A., Olsen, M., Caradoc-Davies, K.M.B., Drake, K. and Ward, V.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hydrk, O., Dellow, R.A., Olsen, M., Caradoc-Davies, K.M.B., Drake, K. and Ward, V.K.
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/organism="Epiphyas postvittana nucleopolyhedrovirus"
/organism="Epiphyas postvittana nucleopolyhedrovirus"
/ob_xref="taxon:70600"
/note="EppoMNPV"
/note="EppoMNPV"
/note="ORF136"
/note="ORF136"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The complete sequence of the Epiphyas postvittana
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'db_xref="GI:15213127"
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'product="Pol"
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                          541 CATCTGTT
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AY043265/c
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114732 CTACGAATCGTAGACTATTTAACTTGAATAGTCTACACTGTTCTATACGCTCCTAATACA 114673
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/db_xref="G1:23476562"
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VKEFTEKCPGMLVGVHCTHGINRTGYMVCRYLMHTLGIAPQEAIDRFEKARGHKIERQ
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NEDVQRFNRTSRNDLISACMQINVHTYMPNATIDMRKQPNCIYFRICQYCHLEADVPS
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SFDCNKFLRSDDMTPVVTTITPKRTADYKITEYVGDVKTIKPSDRPLVESGPLMREAA
                                                                                                                                                                                                                   AY145471 131526 bp DNA circular VRL 07-JUL-2003
Rachiplusia ou multiple nucleopolyhedrovirus, complete genome.
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Boundagh.C. and Harrison,R.L.
Direct Submission
Submitted (28-AUG-2002) Entomology, Iowa State University, Ames,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/db_xref="taxon:80366"
join(131515: .131526,1. .326)
/note="consists of 30 bp imperfect palindromes; hrl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Harrison, R. L. and Bonning, B.C. The nucleopolyhedroviruses of Rachiplusia ou and Anagrapha falcifera are isolates of the same virus J. Gen. Virol. 80 (Pt 10), 2793-2798 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 131526)
Harrison, R.L. and Bonning, B.C.
Comparative analysis of the genomes of Rachiplusia ou and
Autographa californica multiple nucleopolyhedroviruses
J. Gen. Virol. 84 (Pt 7), 1827-1842 (2003)
                                                                                                                                                                                                                                                                                                                                           Rachiplusia ou multiple nucleopolyhedrovirus
Rachiplusia ou multiple nucleopolyhedrovirus
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                               114672 CTACTACACATTGAATTTTTTTTGTAGTGCAAAAAATTACATAT 114630
                                                232 CTACCACACATTGAACCTTTTTGCAGTGCAAAAAGTACGTGT 274
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/note="ptp; rol; acl-like"
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/codon_start=1
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1 (bases 248 to 8029)
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TEMHVHRIMFSGNRGFHMMLKFADGFKIGALKSVREHWYRIFEKPTRLNMRDIRNGSF
AHCMQRAVNMYQDQILQSSKPDELILHFWPDVDKDVFCNPTKQIRAPFSYNHKGTQFS
RCITQQLLEKIQKCSTGCSDGGASTSSISNITH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MHFAVILTILAAQAHAANILAVIPTPAYSHHLVYKAYVQALANK
CHNYTVIKPQILNYVDSNAHWCGHIEQIRADWSSEQYKKLVSSSGAFRKRGVVADETT
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TAFONGLDRAPDTAAAVARHPKYYPNIWKSTPVGGAGALSWRLNWEFELLARYSDK
LIKKIQFGFTTPTIRELRNNVQLLILINIHPVYDNNRPVPSVQYLGGGGHLTQTQPQNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QKTLERQLNASVNGIVYVSFGSSIDTKSIHDEFLQMLVNTFTGLANRTVLWKVDDAVV
SIKLDPWLYTQNWFNQRAVLHKKNTVAFVTGGELQSSDEALHAQVPMVCLPMMGDQF
HHANKLQEFKVARTITAVDVSSGOLILAITDVIVNKKIYQTRWAELRAVIDYDEIAPA
DKAIKFTERVIKFGHDITYPARSLKSPAANLDQSNYFISFPL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAK85577.1"
/db_xref="G1:15213138"
/translation="METPRAMIPSERATPKRAALGTFVKTVVTTTTVSGRGLTRDERNR
/translation="METPRAFYRAMORLVRKKNNIIADLAAQLERRRCRSKGSK
YPAVICQNGVLITISGSGQFVRQRVANMCAVGGBQIFCERRNDCARDRQLIAEALAAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                     /translation="MFD#MFGWWSFNEQHQQHHPLANHFNAQDYKQYAVDRRAQSDLV
NRSVFKCHPPTFKFRYVIDDDNGRCCRVVDFCKGLEINHELMLNCKWDSKHVRHLNEI
                                                                                                                                                                                                                                          KTVLKHI KTLINVNSDKPINAHKLFENQVČARFEQLEGRLETLERVPDA PTMPGVI FPR
DVNKHQHLAVFVNQERGNTQI GFARGQEEY FRKRKLEFEEEDMHKMLETVHPNPQMAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MDLTITLIPISLKNIEEPKRSECFKLTSMREDAEFCLNVKCRSP"
                                                                                                                                                                                                                        VFKTPPVEISPDSMGTVYATKHGLIQILQQLSFEYKDDVLLAIKTDKGYDCDDVRDNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MATYMYTLDRVNLMWNSIAYNNSRKFAFMTLKQRWIHVDRHFDN"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ô
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                                                                                                                                                                                                                                                                                             OCIKDRFISNGYKIKKVSNRRRVIEVDCNINAAKDIVNNVIIS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score .....,
Pred. No. 4.8e-24;
"*:omatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                   /note="ORP11"
/codon start=1
/product="LEF-1"
/protein_id="AAK85575.1"
/db_xref="G1:15213136"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAK85578.1"
/db_xref="G1:15213139"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein id="AAK85576.1"
                                                                                                                       /protein_id="AAK85574.1"
/db_xref="G1:15213135"
                      .6490)
                                                                                                                                                                                                                                                                                                                  complement (6427. .7182)
/gene="lef-1"
                                                                                                                                                                                                                                                                                                                                                                  complement (6427. .7182)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       db_xref="GI:15213137"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/product="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/product="unknown"
TVAEAYNNVLKNNII"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="ORF12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8914. .9528
/note="ORF13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9497. .10123
/note="ORF14"
                                                                                                                                                                                                                                                                                                                                                                                       'gene="lef-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7254. .8732
/gene="egt"
7254. .8732
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/gene="egt"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Matches 131; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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129942
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VLVCKRPSSXYNVIFDSINHQHLKGVYKKTDVQITNYNKYINCICNELRQDEFYAKSS
WIASICCHQRATIFSYTNKQVEMKYHLXNVALVESEDCNEFYPFEPTSDCLICKQKNQ
COMPALEMENT (8223)
/note="roll; ac13-like"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESVLKHVKKLNANSEKFMVTHETFRNBVGNR FEOFEI RIHELDAKLINTLOSAEKLKTA
VVTESQNGTVTFPRDITKHQHLAVFSER I DDR I KLA FVLGQERHFRKRKMR FEDDMEV
LYDGVHPNPILA I QCINEKLYDKHYKI RKI AKRVI DVNCTPNVVKEVI QEVL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="ecysteroid UDP-glucosyltransferase"
/protein_id="AAN28031.1"
/db_xref="G1:23476484"
/translation="WTILCAUALLSTLTAVNAANILAVFPTPAYSHHIVYKVYIEALA
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VTAANYLGLIEMFKDQFDNINVRNFIANNQTFDLVVVBAFADYALVFGHLYDPAPVIQ
DFGRQCKDVYKNLKDVFDVLHAHSMSDKDKNSLMDLLCVMDCEEIDVDCFYY1FEAFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IVKWDSFKCNTHTFKYRYVHSDTNAKCYNVIDFCKGLEIAHDDILDCNWDGDQIYHLN
EIVFHKPSSKRDLNSLGALFATKHGLLEILMQLNFANKSNALLHIQTEGERDDLRDKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="late expression factor - 1"
/protein_id="AAN28070.1"
/db_xref="GI:23476523"
/translation="WLLCNYTQKRVDMWWDAIAYNDSRKYAFWTVNARWIHADRYFDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQLYNYIVQNKVSDVHVKPLDDGGGREWVVDADYKNYVDEHDLMLKIYIGATAFLLF
YEBRVSKWYNYTGNRGFHLMLRFTDKFKTISAQNVRVHRYKVFKPEKDAKLLDSDYIQPGS
YAHCVREAVRLYVEHIQESNFDALTLQYWPDVDRDIFCNVNKQIRAPYSYNYKGTKFFS
RCITKELLDKLKQCYPGYGGGGPVTTTATTSSPLKIGLIQTTTKSTT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IAPCYGLAENFDTVCAVARHPVYHDNIWRNNFDDTEANVMTEWRLYKEFKILANMSNA
LLKQQFGPNTPTIEKLRNKVQLLLINLHPIFDNNRPVPPSVQYLGGGIHLVKNAPSTK
LNPVINAQMNKSKSGTIYVSFGSSIDTKSFANEFLYMLINTFKTLDDYTILWKIDDEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VKNITLPVNVITQNMFNQRAVLGHKKMVAFITQGGLQSSDEALEAQIPMICLPMMGDQ
PYHAHKLQQLGVARALDTVTVSSDQLTVAINDMLFNAPIYKKHMAELYALINHDKATF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MLSWLWNWWMWSSDNDSDDVIAVEDRFNPDDYKKYHINAQQWSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation="MLFTIIVLVFLRGALCGCALSAFINAHQPKQVIIVPGRSKAKHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPLDKAIKFTERVIRYRHDISRQLYSLKTTAANVPYSNYYMYKSVFSIVMNHLTHF"
11578. .11745
/note="rol3a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         171
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Pred. No. 8.6e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(9128. .9931)
/note="lef-1; ro12; ac14-like"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10045. .11565
/note="egt; rol3; ac15-like"
/codon_start=1
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                                                                                                                                                                          protein_id="AAN28100.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAN28055.1"
/db_xref="GI:23476508"
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/db_xref="GI:23476614"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="unknown"
/protein_id="AAN28087.1"
                                                                                        note="rol0; ac12-like"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="ro14; ac16-like"
/codon_start=1
                                                                                                                                                                                                                db xref="GI:23476553"
                                                                                                                                                    product="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         product="unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                             codon start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db xref="G1:23476546"
/translation="MAVIFNNKQLLADDSIENGGELFLLNGSYSILENYVNPVLLKNG
NVDPALFKNIDLEFAAYYAGNILYKTDDFKSIDYINLIKATHSEELPENSTVLNFTK
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ASSLCENKIILSQINCESFENDFKHYLDDYNYAFSIIDNSTNVLVAFGLYC"
                                                                                                                                                                                                   /trānslation="MANALYNVWSPLISASCLDKKATYLIDPDDFIDKLTLTPYTVFY
NGGGLIKISGRLKYMLITPPPTINEIKNSNFKKRSKRNICMSKGCABGKGNVUDMLNSK
INMPPCIKKTLGDLEKENNVPRGGWYRKRFILMCYTANVNSCAKCENRCLINALTHFYN
HDSKÇVGEVMHLLIKSQDVYKPPNCOKMKNVDKLCPFAGNCKGLNPICNY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /trānslation="MPDYSYRPTIGRTYVYDNKYYKNLGSVIKNAKKKHLIEHEEBE
KHLDPLDNYNVAREDPFLGPGROKKTTLFKEIRNVKDTWKLIVWNGGREFMRETWTRP
VEDSFPIVNDGEVMDVFLVYNLRPTREPRRCYKFLAQHALRWDEDYVPHEVIRIVEPSY
VGMNNEYRISLAKKGGGCPINNIHEBYTNSFESFVGRVIWENFYKPIVYIGTDSGEBEE
ELLIEVSLVPRVKEFAPDAPLFTGPAY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="myneryesvosylennennkidahoflervdtaeaoiiknniyd
ntvvl.nrdvl.ini.kl.andvpdnkaenkyddsevsrhynavvrmkr.ivigvrdpslro
st.vniiavilelliniiknoseitmliadpydd.snynielbloallersrresvvop
tapavptiareqiteroiitgapppsspasnipappppppppppspspred
tepepvaplidroqulleairneknytrlrpvkpktivettilelptulpktfeeprp
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KYLÖKTISAHNFNADEIKYHQLMSDHPIKIYFRHGSINNQVIVWDYIDCPDLFET
LQIKGELSYGUSNIIRQLCBALNDLHKHNFIHNDIKLENVLYFFRALDRYVCDYGLC
KHENSPSYHOCTLEFRSPEKIRHYNYARSFDWYAVGYLTYKLLTGGRHPFEKSEDEML
DLNSMKRRQQYNDIGVLKHVRNVNARDFVYCLTRYNIDCRLTNYKQIIKHEFLS"
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MSCIERDVTAMRRIAGGSCTFDEAVXMIDACDSIKSLSHWFGTSEWMGINDNYREVLE
DIDAVVPVSVVQNGWDIFSLNNFEREISQDMLDCLQIILGRFBYFRRNGKLIRLSTV
FNDNNNVVGWWYNKFCVVTYYHRINYQSVPAELAPRLSEAVKKFIRLRKSDYDDRLHL
DESYNCPRVIAEIYGRFCGIGKEHFSKHKLSCMHILFQYLRGKTTQEEESFPCYRVIK
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SNAANKPVRXVQSLENVFTSQLYTNNDEKRYTKAHDILNDVEALLQNKTYGTNIDKA
RLILQDLASFVTLSRPLDSFVIGSBKQPLFETNRNLFYKSIEDLIFKFRYKEAENHL
IFALTYHPKDYKFNELLKYVQQLSVNQQRTESSA"
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                                                                                                                 <u>.</u>
                                                                                                                 product="late expression factor
                                                                                                                                                                                                                                                                                                                                                       'note="orf603; ro5; ac7-like" (codon start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 product="protein kinase - 1"
                  1756. .2388
/note="lef-2; ro4; ac6-like"
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/note="pk-1; ro8; ac10-like"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3230. .3967
/note="polh; ro6; ac8-like"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (3997. .5625)
/note="orf1629; ro7; ac9"
                                                                                                                                          protein_id="AAN28095.1"
db_xref="GI:23476548"
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db_xref="GI:23476480"
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db_xref="GI:23476534"
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/db_xref="GI:23476522"
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/db_xref="GI:23476507"
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complement (6515. .7534)
/note="ro9; ac11-like"
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product="ORF1
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Autographa californica nucleopolyhedrovirus clone C6, complete
                                                                                                                                   07-MAR-1997
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Ayres, M.D., Howard, S.C., Kuzio, J., Lopez-Ferber, M. and Possee, R.D.
The complete DNA sequence of Autographa californica nuclear
Virology 202 (2), 586-605 (1994)
94303173
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/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172 CTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 133894;
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Autographa californica nucleopolyhedrovirus
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
                                      166 CTACTACACTATCAACTTTTTTGCATTACAAAAAAGTTCATTTTTGC
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Bishop,D., Possee,R. and Ayres,M.
AUTOGRAPHA CALIFORNICA COMPLETE GENOME SEQUENCE
PACHAL: WO 9601320-A 1 18-JAN-1996;
NATURAL ENVIRONMENT RES (GB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 6;
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Location/Qualifiers
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/organism="unidentified"
                                                                                                                                   133894 bp
Sequence 1 from Patent W09601320
                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="unassigned I
/db_xref="taxon:32644"
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Kuzio, J.
                                                                                                                                                                                    A48542.1 GI:2302312
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Identification of the very early transcribed baculovirus gene PE-38 J. Virol. 65 (2), 805-812 (1991) 91101290
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early
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Original source text: Autographa californica nuclear polyhedrosis virus DNA, and cDNA to mRNA, isolated from Spodoptera frugiperda. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          californica nucleopolyhedrovirus"
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18.0%; Score 101.4; DB 14; Length 1511;
Best Local Similarity 75.4%; Pred. No. 4.4e-21;
Matches 126; Conservative 0; Mismatches 41; Indels 0;
                                                                                                                                                                    VRL
                                                                                                                                                                                  Autographa californica nuclear polyhedrosis virus major
protein (PE-38) gene, complete cds.
                                                                                                                                                                                                                                                major early protein PB-38.
Autographa californica nucleopolyhedrovirus
Autographa californica nucleopolyhedrovirus
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
1 (bases 1 to 1511)
                                                                                 129881 CTACTACACTATCAACTTTTTGCATTACAAAAAGTTCAT 129841
                                                                                                                                                                    linear
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                                                    CTACCACACATTGAACCTTTTTGCAGTGCAAAAAGTACGT
                                                                                                                                                                    DNA
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db_xref="G1:332471"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Autographa ce
/mol_type="genomic DNA"
/db_xref="taxon:46015"
complement(1, .294)
                                                                                                                                                                    1511 bp
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/gene="IE-N"
352. .1453
/gene="PE-38"
352. .357
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379. .1453
/gene="PE-38"
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/gene="PE-38"
1433. .1438
/gene="PE-38"
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/translation="MANASYNVWSPLIRASCLDKKATYLIDPDDFIDKLTLTPYTVFY
NGGYLWKISGLRLYMLITAPPTINEIRNSNFKRSKRNICMKECVEGKKNVUDMLNNK
INMPPOIRKILNDLKENNVPRGGMYRKRFILNCYIANVYSCAKCENRCLIKALTHFYN
HDSKCVGEVMHLLIKSQDVYKPPNCQKMKTVDKLCFFAGNCKGLNPICNY"
complement (3759, .4364)
/gene="Ac-ORF603"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /profein id="AAA66637.1"
/db_xref="G1:559076"
/translation="MAVIFNKQLLADNSIEKGGELFLFNGSYNILESYVNPVLLKNG
/translation="MAVIFNKQLLADNSIEKGGELFLFNGSYNILESYVNPVLLKNG
VIELEBAAYAGNILYKTDDPKFIDYINLIKATHSEELFENSTVNYRKTWRSGTIH
PIKKDIYIYDNKKKFILTDRYIYGYDNNYVNFYEKKNEKEFEEDDKASSLCENKII
LSQINCESFENDFKYYLSDYNYAFSIIDNTINVLVAFGLYR"
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complement (5287. .6918)

/note="axnonym: AcOrf-9; Ac-61K; Ac-vp78"

complement (5287. .6918)

/gene="ac-oRF1629"

/note="61K; vp78; required for virus replication; 60713 Da primary translation product"
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AAPAPVPTIVREQTKPEQIIPAAPPPPSSPVPNIPAPPPPPPSMSELPPAPPMPTEP
QPAAPLDDRQQLLEAIRNEKNRTRLRPVKPKTAPETSTIVBVPTVLPKETFEPKPPSA
   SFDCNKFLRSDDMTPVVTTITPKRTADYKITEYVGDVKTIKPSNRPLVESGPLVREAA
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TATDPLDNTLVAEDPFLGFGKNQKLTLFKEIRNKPOTWKLVGWKGKERYREYWRF
MEDSFPINNDGWNDVFLVNAMRFTRENRCYKFLAGHALRCDPDYVEHDVIRIVEPEN
VGSNNEYRISLAKKGGGCPIMNLHSEYTNSFEQFIDRVIWENPYKPIVYIGTDSAEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="winkryesvosylennrnnkidahoffervdtaeaqiiknniyd
ntvvlardvilnilklandvfdnkaymyvddsevsrhynavvkmkrlvigvrdpselro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="polyhedrin; 28642 Da primary translation product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="synonym: AcOrf-7"
complement(3759. .4364)
/gene="Ac-ORF603" peptide; 23612 Da primary translation
                                                                                                                                                                                                                                                                    note="LEF2; 23926 Da primary translation product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="Ac-pk-1"
/note="PK1; 31978 Da primary translation product"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
/product="viral capsid associated protein"
/protein_id="AAA66639.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product="major occlusion body protein"
protein id="AAA66638.1"
db_xref="GI:559077"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIFALTYHPKDYKFNELLKYVQQLSVNQQRTESSA"
                                                                                                                                                                                                                                                                                                       codon_start=1
product="late expression factor 2"
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/gene="Ac-pk-1"
/note="synonym: AcOrf-10"
                                                                                                                                                                                                                                                                                                                                                                             protein_id="AAA66636.1"
db_xref="G1:559075"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'note="synonym: AcOrf-8"
1520. .5257
                                                                                                                                                   note="synonym: AcOrf-6"
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                                                                         3089. .3721
/gene="Ac-lef2"
                                                                                                                                                                                      3089. .3721
/gene="Ac-lef2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'codon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAA66631.1"
/db_xref="G1:559070"
/tb_xref="G1:559070"
/tb_xref="Inplanger" | The protect | The protec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="baculovirus repeated ORF"
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/brotein_id="AAA6632.1"
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DKAIRWHVDNKYKSLEEQTIQNGGFFKFGEDTFNLRYVLEBESKQLVTKLIATFEGTOLIMKS
KLPYAIELQEWILLEEVIPQVLCTGKYDPAIKQREESKQLVTKLIATFTHTNALQAV
VAQKTEELYKKQEFIRRIVAIKOKQIEAKDLQVTRVWTDLNRYYTGFQETMQKKDEIM
QKKDAQYTDLVAKVVDLSDRAVQYPADKRKHPVLCYTRDGTTFTAITGQKTYVENQKH
KRNINVANITVVENIRENPTYDWNNATDRLQAKRSKRSIVLVRWKKRNNLKIG"
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SEDVQRFNRTNRNDLISACWQINVRTYMPNATIDMRKQPNCIYFRICQYCHLEADVPS
PDDHSVYRYLCVACGTPLVIDHPLDVFGHTEEGVNELLEVQRVNAGGEL"
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                                                                                                                                           /note="5 Copies of 30 bp imperfect palindromic sequence;
the EcoRI site in the first palindrome is at residue 1 of
the linearized genome"
                                                                                                                                                                                                                                                                                                                                                                                                                                           503. 1009
/gene="Ac-ptp"
/note="PTP; 19288 Da primary translation product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="BRO; 37769 Da primary translation product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="CTX; 5590 Da primary translation product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (2295. .2750)
/gene="AcOrf-4"
/note="17577 Da primary translation product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene="AcOrf-5"
note="12435 Da primary translation product"
                                                                                                                                                                                                                                                                function="enhancer; replication origin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phosphatase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        product="conotoxin-like peptide"
                                  /clone="C6"
join(133883. .133894,1. .445)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/product="protein tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        product="AcOrf-4 peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        product="Acorf-5 peptide"
protein_id="AAA66635.1"
db_xref="GI:559074"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="synonym: AcOrf-3"
complement (2084. 2245)
                                                                                                                                                                                                                                                                                                                                                                                                                note="synonym: Acorf-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="synonym: AcOrf-2"
complement(1041. .2027)
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/db_xref="GI:559072"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein id="AAA66634.1"
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xref="taxon:46015"
                                                                                                                                                                                                                                                                                       /rpt_type=dispersed
503. .1009
                                                                                                                standard_name="hr]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="Ac-bro"
                                                                                                                                                                                                                                                                                                                                                                         gene="Ac-ptp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'gene="Ac-bro"
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                                                                     repeat_region
                                                                                                                                                                                                                                                                                                                                      gene
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FVAPSPOATQTPSPRQTFAAPSPVPAESPQPTRAFPTPEGTLSRGAADEFEYPGGTSV NGVNLATTLKPPVPPRPAHLSRPWFWFPVPGKVTGNTPPPPNGTSPQPGVNVPPPPVAP PENVMPPPPPNVPPPPPLANLLIDAMMSEPRKGATDRSALFEDIKWGATLKKAQPVE PENNWPPPPPPNV ORTGATLKKTGALBENLGKPKKGREGILGVLYNTLGSRRGGIDSE RSDVATSESTSGPPSADTFAADKASKSELKTAAAHLYNFAKOSKLYNIQKVNNSELTKI LENVGPLLKRSPRTABKASKSELKTAAAHLYNFAKOSKLYNIQKVNNSELTKI LENVGPLLKRSPRTAENVEKANAGLYLFRQHVTLPKNALDAQPAPELYAADAPQFYVQ IEDLLFAGRYDDARAFICAVDAPEDMKLKKFLTVANQLSTRGQ"
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KHLDPLDHYNVAEDPPLGPGKNQKLTLFKEIRNVKEDTWKLIVWNSGKEFLRETWTRF
KEDSFPIVNDGEWMDVFLVINLRPTRPNRCYKFLAQHALRWDCDYVPHEVIRIVEPSY
VGMNNEYRISLAKKGGGCPIMNIHSEYTNSFESFVNRVIWENFYKPIVYIGTDSGEEE
EILIEVSLVPKVKGFPADAPLFTGPAY"
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VLASTVARTENLLRSDAVNDVETTVLSGDFYEEYSRYATRQYVSTDTLPPPPPLTPPT
PETTQAFVAPSPPPAQAFVAPSPPPAQAFVAPSPPPAQAFTAPSPQPTFVAPPSPPPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /produčt="viral capsid associated protein"
|protein id="AAQ91783.1"
|db_xref="GI:3749384"
|translation="wdRQYQSYKSYLNNNAHNAIDADAFFQLVAGPEAHNLKRGLFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MADSTNRILRLFYRWSSKTGASLENQADLECLYDLERFVGAHMN
KQIETSCKKKKQAEERAESAALKRVELAADRMAMQAKAAPYCADDGRWSTLSQQQLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     On or before Oct 8, 2003 this sequence version replaced gi:1117788, gi:2581770, gi:174838, gi:4092491.
Location/Qualifiers
1. .131158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (20-JUN-2003) Molecular Virology, Great Lakes Forestry Centre, 1219 Queen St. E., Sault Ste. Marie, Ontario PGA 2E5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (note="ORF 1; ph Op3/Ac8; major occlusion body protein"
                                                                             1 (bases 80268 to 81693)
Li,X., Lauzon,H.A., Sohi,S.S., Palli,S.R., Retnakaran,A. and Arif,B.M.
Molecular analysis of the p48 gene of Choristoneura fumiferana multicapsid nucleopolyhedroviruses CfMNPV and CfDEFNPV
J. Gen. Virol. 80 (Pt 7), 1833-1840 (1999)
                                                                                                                                                                                                                                                                                                        4 (bases 1 to 131158)
Li,X., Barrett,J., Pang,A., Klose,R.J., Krell,P.J. and Arif,B.
Characterization of an overexpressed spindle protein during a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Choristoneura fumiferana defective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lauzon, H.A.M., Jamieson, P.B., Krell, P.J. and Arif, B.M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="ORF 149; 1629 capsid Op2/Ac9"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleopolyhedrovirus"
/mol type="genomic DNA"
/db xref="taxon:74660"
join(129349. .131158,1. .20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="ORF 3; lef-2 Op6/Ac6"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="polyhedrin"
/protein_id="AAQ91696.1"
/db_xref="G1:37499297"
  Virus Genes 13 (3), 229-237 (1996)
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/db_xref="GI:37499343"
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/codon at----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .1858)
                                                                                                                                                                                                                                                                                                                                                                                                                Virology 268 (1), 56-67 (2000) 20149221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 131158)
                                                                                                                                                                                                                                                                                                                                                                                               baculovirus infection
                                                                                                                                                                                                                                                                              10423153
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AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
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MEDLINE
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JOURNAL
                                                                                                             AUTHORS
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                                                                                                                                                                    TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132384 AATTTTTTGCAATGCAAAAAGTTCACTTTTGCCTGACACTCCATATACAGTACAATCT 132325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        132324 CTACAAATCGTAGACTATTTTATTAGAATAGTCTACACTGTACGATACGCTCCCAATATA 132265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleopolyhedrovirus.

1 (Dases 11500 to 13512)

Barrett,J.W. Krell,P.J. and Arif,B.M.
Characterization, sequencing and phylogeny of the ecdysteroid
UDP-glucosyltransferase gene from two distinct nuclear polyhedrosis
viruses isolated from Choristoneura fumiferana
J. Gen. Virol. 76 (Pt 10), 2447-2456 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The putative LBF-1 proteins from two distinct Choristoneura fumiferana multiple nucleopolyhedroviruses share domain homology to eukaryotic primases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QIDAVVPSVRVQNGWQI FSLINNFEREI SQDMLDCLQI ILGRFEYFMRNGKLLRI ANV 
PRINDIDVOPWWYNKFCVYTYNRI NIRSOPABLEIVPRLSEBAVKGRI RIKKSDYDDDRLHV 
DESYNCPRVI AEMYGRFCGI GKEHFSKHKLSCMHI LFQYLRGKTTQERKS FPOTRVIT 
DFGRQCKDVYKNLKDVFDLLHAHSMSDKDKNSLMDLLCVMDCEEI DVDCFYY I FESFL
                                                                                                          KLYLQKTISAHNFNADEIKVHQLMSDHPNFIKIYFNHGSINNQVIVMDYIDCPDLFET
LQIKGELSYQLVSNIIRQLCEALNDLHKHNFIHNDIKLENVLYFEALDRVYVCDYGLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /trānslation="mSLAaKLIIXNYYAKYNEVHDVYGESYHHYRIVQEYLSESYVNG
MSCIERDVTAMRRLKSGSCTFDEAVKMIDAGDSIKSLSHWPSTSETMGIDDNVREVLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                translation="MATTNATLQTLVQFYENCKNVKTRYKIINGRFGKISILSHKPTS"
                                                                                                                                                                    KHENSLSVHDGTLEYFSPEKIRHTTMHVSFDWYAVGVLTYKLLTGGRHPFEKSEDEML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             circular VRL 08-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barrett, J.W., Lauzon, H.A., Mercuri, P.S., Krell, P.J., Sohi, S.S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Cfdefnpv)
                                                                                                                                                                                                                                                                            /note="2 Gopies of 30 bp imperfect palindromic sequence" /function="enhancer; replication origin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Choristoneura fumiferana defective nucleopolyhedrovirus complete
                                                                                                                                                                                           DINSMKRRQQYNDIGVLKHVRNVNARDFVYCLTRYNIDCRLTNYKQIIKHEFLS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 101.4; DB 14; Length 133894; Pred. No. 1.2e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132264 CTACTACACTATCAACTTTTTTTCCATTACAAAAAGTTCATTTTTGC 132218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Choristoneura fumiferana defective nucleopolyhedrovirus
Choristoneura fumiferana defective nucleopolyhedrovirus
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                   complement (7899. .8921)
/gene="AcOrf-11"
/note="40093 Da primary translation product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTACCACACATTGAACCTTTTTGCAGTGCAAAAAAGTACGTGCGGC 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="AcOrf-11 peptide"
/protein_id="AAA66641.1"
/db_xref="GI:559080"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                            /protein_id="AAA66640.1"
/db_xref="G1:559079"
                                                                                                                                                                                                                                                                                                                               /rpt_type=dispersed
complement (7899. .8921)
/gene="AcOrf-11"
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                                                                                                                                                                                                                                                  /standard_name="hr1a"
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75.4%;
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Best Local Similarity
Matches 126; Conserv
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VERSION
KEYWORDS
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TITLE
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AY327402
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125537 AACATTATTGCAGTGCAAAAAGTTCACTTTTATATCGCACCCTATATACACATACGAAC 125596
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                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
/product="actin rearrangement inducing factor"
/protein_id="AAQ91678.1"
/db_xref="GI:37499279"
/translation="MLAQINYILQLVLHAALYTITLIAFVFSLMGTINYKYAFLLELN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVCWTLFVVFQPQIYKNGHVPVLDARYRDYDRNSLCWSNIVSDTYEVHDTNAIRTDFN
CVYRHDFVKKCVGCRMEVRHDEPTVFNQNQCALIMMVMMTAVLQFWNMYVQRKEMRYK
PTPVKTLYFESAPLKEQDTADEEEEQQSSFRMLEIISEPRVQFQFPESSSLDRLSSPP
                                                                                                                                                                                           DPGASYFFVGEGDTYVVNGHKLAVGGYCTTNSVPRDCNRETSVVLMSLNQWTC1AEDP
RYFAGTSNWTQLAGRQHFDR1LPGQSDRNVLFDRLLGREVNVATNTFRRSWDELLEDG
                                                                                                                                                                                                                                               TRRFEMRCNARDINNNÄLMFVNPLNPLECLPNVCTNVNYVHTSVRPNFETGECDCGDEA
VTRVRHVVPGDRSSVCASIVDGLDTTTASHRPRVECVNTYTSIGNFSNNKLLCPSDTF
DSNTDAAFAFEVPGSYPLSGNGLDEPTHRFFLDTRSRIRYNDVRGLIN"
                                                                                                                                 /trānslation="myrilivlplpallyivwppyqayqHiqtaqHDyndtldtbkmb
YISSVMRRRHYVPMEALPSVQFDTNLGTLAGETLKCMSVPLYVTEIDLPFFDCTQVCB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNGHSVINLSVLTAFLLGPCVFTTTTWAIYKFLLCYKRAEMHSNFYMKTIISLAHVMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAT 17-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATAC
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WONKYUNG KANG, NORIKO IMAI, SUMIKO GOMI, SHOGO MATSUMOTO PC 15/09, A01K67/033, C12N7/04
From 100,001 to 128,413 of BnNPV genome DNA Key
source 1. .28413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BD187790 28413 bp DNA linear PAT 17-JUI
A virus in which a gene for controlling an insect behavior is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 131158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIVOSSSSPNSPDSGIDYDIPOPFYSVPNKVVCKYLCRTHATLCA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kangwill, M., Gomi, S. and Matsumoto, S. A virus in which a gene for controlling an insectent: 19 2003024662-4 3 28-3AN-2003;
THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH OS Bombyx mori nucleopolyhedrovirus
PN JP 2003024662-A/3
PD 28-JAN-2003
PP 10-JUL-2001 JP 2001209305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231 ACTACCACACTTGAACCTTTTTGCAGTGCAAAAAGTAC 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 100; DB 14;
Pred. No. 3.3e-20;
                                                                                                                                                                                                                                                                                                                                                               /note="ORF 11; arif Op19/Ac21"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (9013. .9327)
/note="ORF 12; Op18/Ac19"
note="ORF 10; Op20/Ac20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="unknown"
/protein_id="AAQ91753.1"
/db_xref="G1:37499354"
                                                                             protein_id="AAQ91663.1"
db_xref="GI:37499264"
                                                   'product="unknown"
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80.6%;
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                                                                                                                                                                                                                                                                                                                                   7898. .8863
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C12N15/
CC Fr
FH Ke
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Best Local Simi
Matches 129;
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ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MYDANQIDENLFVGGYYGNNEAMLQFIKKHDIESVISLIDSDVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / LTAIRLALLOIS-WEPGRWINYTTCGKVIEGTNLICFKVPLKQEVFEYVTNDEDRWT
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/notton similar to Ac hrla"
/function=enhancer; replication origin"
complement (6723. .7871)
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protein id="AAQ91726.1"
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                                                                                                                                                                                                                                                                         protein_id="AAQ91760.1"
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/gene="lef-1"
/note="31098 Da primary translation product"
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Bombyx mori nuclear polyhedrosis virus isolate T3, complete genome.
L33180
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Gomi,S., Majima,K. and Maeda,S.
Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus
J. Gen. Virol. 80 (Pt 5), 1323-1337 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bombyx
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Submitted (19-MAX-1994) Department of Entomology, University of
California, Davis, CA 95616, USA
4 (bases 1 to 128413)
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                                                                                                                                                                                                                                                                                                  CTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACA
                                                                                                                                                                                        Gaps
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Kamiteh.SG. and Maeda.S.
Sequencing of the putative DNA helicase-encoding gene of the lmori nuclear polyhedrosis virus and fine-mapping of a region involved in host range expansion grant 190 (1), 173-179 (1997)
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                                                                                                                                                Length 28413;
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Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bombyx mori nucleopolyhedrovirus
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1. .738
           Location/Qualifiers
1. .28413
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                                                                                                                                              Query Match
Best Local Similarity 72.5%;
Matches 121; Conservative
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complement (3248. .4270)
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FNPNSDAVGWWYNKFCVITYVHRIMHRSVPAELVPRLSEAVKKFIRLSKSDYDDRLHV
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KTAIVTESKNGTVTP PRDITKHQHLAI FSERIDDRIKLAFVLGQERHPRKRKMR FEDD
MEVLYDGVHPNPLLAIQCINEKLYDKHYKIRKIAKRVIDVDCTHNVVKEVIQEVL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QPAAPAPVPTIVHEQTKPEQIIIPAAPPPSSVPNIPAPPPPPPPPFSSMSELPPAPP
MPTKPQPAAPLDDRQQLLEAIRNEKORTRLRPVKPKTAPETNTIIEVPTTVLPKEPKP
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DFGRQCI DVYRDLKDVFDLLHAHSMSDKDSKNSLMDLLCVMDCEEI DVDCFYY I FESFL
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/note="32442 Da primary translation product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="Orf 4"
/note="39756 Da primary translation product"
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/note="393]5 Da primary translation product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="Protein Kinase=PK1=AcMNPV orf10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      product="Orf1629=pp78/83=AcMNPV orf9"
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/product="AcMNPV orf11"
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complement(3248. .4270)
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complement (4605. .5600)
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/translal.ion="WTILCWLALLSTLTAVNAVNILAVFPTPAYSHHIVYKVYIEALA
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VAANYLGILEMFKOOFDNINVRNILANNOTEDLVVVEAFADYALVFGHLVDPAPVIO
IAPGYGLAENFDTVGAVARHPVHPNIWRNNFDDFTKANLMTEMRLYKEFKILANMSNA
LLKQQFGPDTPTIEBLRNKVQLLLLMIHPITPNINKPVSFPSVQTGGGTHTVKSAPLTK
                                                                                                      AAQLYSYIVQNKVSDVHVKPLDDGGGREWVVDADYKNYVDEHDLMLKIYIGATAFILF
YTERNVSKWYTGNRGPHUMLKFTDFRKTISAGNVRVHRYKAFEKPAKLDSDCIQPGS
YTERNVSKWYIPHODSNLDAFILQYWPDVDRDIFCNVNKQIRAPYSYNKGTKFS
RCITKELLDKLKQCYPGYGIGGCGPVTTTTTTTPPSPPKIGSIQTTTKSTT
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produce di 3AC6690.1"
db xref="GI:3745643"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSPÖTDAKMIKSKSGALYVSFGSSIDTKSFANEFFYMLINTFKALDNYTILWKIDDEV
VKNITLPANVITQNWFNQRAVLRHKKMAAFITQGGLQSSDEALEAGIPWVCLPMMGDQ
FYHAHKLQQLGVARALDTVTVSSDQLLLAINDVLFNASTYKKHMAELYALINNDKATF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MNSVHTRLCASSNOPAPFKKRQLAVPVGSVNSLTHTITSTTVAS
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EYVFCQARADGDKDRQALASLLIAAFGPRVIVYENSRRFEFINPDEIASGKRLIIKHL
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SVLVNNVVKFIKVDKNYNVTKKNNVTKKNNVTFTGRQLLIILFFKFK"
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                                                                                                                                                                                                                                                                                                                              note="57044 Da primary translation product"
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/gene="Orf 7a"
7940. - 171
/gene="Orf 7a"
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product="LEF-1=AcMNPV orf14"
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complement (9387. .10457)
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/gene="bv/odv-e26"
8067. .8756
/gene="bv/odv-e26"
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/gene="Orf_9"
8725. .9357
/gene="Orf_9"
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/gene="egt"
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122172
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OHYABLIOUTRQIYUSDPYTDNALKCYQNGAYBLNGQIDLHLNHHIKCIKTYQYNDEFDLV
RPALQIDITSAYGVDEYTDNCVKITTAPLSFNVFFVNVRIMKRPFNADRCIKNFSLLG
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Qiu,W., Liu,J.J. and Carstens,E.B.
Studies of Choristoneura fumiferana nuclear polyhedrosis virus gene
expression in insect cells
                                                                                                         NEYHTIVSSLORVINDQLMCLLKDI FTNKFDYKI KRRINHLKRLFANLPAESYNSCVN
DLTDMYLYKEQNETI TNFVKKI LDI SGPDLGCRKLMRI YLNTDTFRGQL PAYLTHYVN
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Xie,W.D., Arif,B., Dobos,P. and Krell,P.J.
Identification and analysis of a putative origin of DNA replication
in the Choristoneura fumiferana multinucleocapsid nuclear
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: nuclear polyhedrosis
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                                                                                                                                                                                                                                                                                                                                                                           231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF512031 129609 bp DNA circular VRL 27-MAY-200-
Choristoneura fumiferana MNPV polyhedrin, complete genome.
AF512031 AF177329 578506 S81690 U10441 U18677 U26676 U26734 U53854
U57401 U59008 U70432 U72240 X65395 S46001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identification, localization, transcription, and sequence analysis of the Choristoneura fumiferana nuclear polyhedrosis virus DNA
                                                                                                                                                                                                                                                                                                                    CTACGTTTCGTAGACTATTTTACATAGTCTACACCGTTGTATACGCTCCAAATACA
                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genome of
                                                                                                                                                                                                  DB 14; Length 128413;
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Choristoneura fumiferana MNPV
Viruses; dsDMA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LUCHTISCATION Of Bent DNA and ARS fragments in the Choristoneura fumiferana nuclear polyhedrosis virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTACCACACATTGAACCTTTTTGCAGTGCAAAAAAGTACGTGTCGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 129609)
Lee,H.Y., Arif,B., Dobos,P. and Krell,P.
Identification of bent DNA and ARS fragments
                                                                                                                                                                                                                                             46;
                                                                                                                                                                                               Score 93.4; DB 14
Pred. No. 4.5e-18;
0; Mismatches 46
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                                                                                                                                                      YPHKNLCDQNWKRFMSCIFSLY"
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Virology 209 (2), 409-419 (1995)
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Virology 209 (2), 538-549 (1995)
95297155
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AF512031/c
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YLMPECGTPLVIDHPLHVFGDTEEGVNELLEVQRINAGGDL"
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VDRVYTNFHSHKNRMVYGQLYSFALSNFSLANQIYIGAPIFEKERMVSVITARHEDYK
NKLVIYPVTGISARGLVSGQINFDLQILTQKLLEGSSVYGKMQLPYKALKDYAISTNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MYDANQIDKYIFVGGYYGDDKAMLQFIKKYDIASVISLINADVG
PIRQALGLPAGEHIHVYCEDAPTCVALPNAMFALYEYMTRRIGEGKRVLIHCYAGESR
SAALVVYYYMSRQMSYEEALSLVKNKRRVAISNHFVRFLASKCSYKFVNNVLKIRVS
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/db_xref="G130269987"
/translation="MFPDRWHEFTPCGRVIDGTRLICFKVPLSAELFEYVTNDEDRWT
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VDEFQDRCPTMLVGVHCTHGLNRSGYLVCRYMVDKLGVSPADAI I RFEEARGHKI ERA
DLHCLYDLERFVGAHLNKRCDAKAKKNKCAEKAALKRVQI SADRHALEAAAAPI DADD
GÇWSKLTSAQLDEI AREKDI VDRI YQLQLKQDRLI KMDGLKKQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           'translation="MTRPTMRNAAAVAADYDREQLRRDLNSLRRSVHELCTRSTTGFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CNRFLDGVDKAPAVIIKPAAAGQHSSLICDKV"
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/codon_start=1
                                                    complement(1251. .1859)
/note="ORF3; lef2; Ac6/Op6"
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/db_xref="GI:30269983"
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/note="ORF10; Ac11/Op11"
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                                                                                                                                                                                                                                                                                                   complement (1862, .2092)
/note="ORF4; Ac5/Op7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (4198. .4731)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2137. .2568
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                                                                                                                                                                                                                                                                                                                                                                                       'product="unknown"
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/note="ORF6;Ac2"
                                                                                                        codon_start=1
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                                                                                                                                                                                                                                                                                             Lapointe, R., Back, D.W., Ding, O. and Carstens, B.B.
Identification and molecular characterization of the Choristoneura funiferana multicapsid nucleopolyhedrovirus genomic region encoding the regulatory genes pkip, p47, lef-12, and gta
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EDSPIVNDQBVMDYFLVVNRRPTRPRKCYKFLKQHALRWDCDYVPHVIRIVESYR
GMNNEYRISLAKKGGGCPIMNIHAEYTNSFESFVNRVIWENFYKPIVTIGTDSGEEEE
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GRHKVVPKSKHVQGLESNLQLLVGVSKHGKMAASDQKILELFYRWSSQTGCEMLDDEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (13-MAY-2004) Department of Microbiology, University of
Guelph, Chemistry and Microbiology Building, Guelph, ON NIG 2W1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (13-MAY-2002) Department of Microbiology, University of Guelph, Chemistry and Microbiology Building, Guelph, ON NIG 2W1,
                                                                                                                        Identification, molecular cloning, and transcription analysis of
the Choristoneura fumiferana nuclear polyhedrosis virus
spindla-like protein gene
Virology 223 (2), 396-400 (1996)
96400202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carstens, B.B., Liu, J.J. and Dominy, C.
Identification and molecular characterization of the baculovirus
CfMNPV early genes: ie-1, ie-2 and pe38
Virus Res. 83 (1-2), 13-30 (2002)
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de Jong, J. G., Dominy, C.N., Lauzon, H.A., Arif, B.M., Carstens, E.B. and Krell, P.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          de Jong, J.G., Dominy, C.N., Lauzon, H.A., Arif, B.M., Carstens, E.B. and Krell, P.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence update by submitter
On May 13, 2004 this sequence version replaced gi:30269978.
Location/Qualifiers
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complement (838. .1449)
/note="ORF2; Op5"
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/db_xref="G1:30269980"
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/db_xref="taxon:208973"
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  217 (2), 564-572 (1996)
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                                                                                                      Liu, J.J. and Carstens, E.B.
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Unpublished
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  Virology ; 96183379
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COMMENT
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Search completed: May 10, 2005, 05:52:38
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Matches 119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (18-FEB-1993) Gentaro Yamamoto, Nagoya University Faculty
of Agriculture, Dept. of Agricultural Chemistry; Nagoya, Aichi
464-01, Japan (Tel:052-781-5111(ex.6238), Fax:052-781-4447)
Submitted (18-FEB-1993) to DDBJ by:
                  /trānslation="MHSVRNLFDSNMSLSSKLLVYAYYGAFNLLHEKYGESYHLYRIV
HEHLTETYVSNASCVRRDIATARCFENGFCFNLARQLLDVTDVAARLAAWYNRGDKTG
LCANVQLALABIDKYAPLEKRVSIGNNIFALDTIADIPSNALDDFQTIIYEGFKDFVD
                                                                                 MINILAHVADVFDPDEKIKAEGWWYYKECVLTYMHRLTVNAVPTELMTRLQDAVIKFVQ
PQNKGNCAPAMANVYGRFCGIGRKHFSQHKAASMYILFQYMRNNLTPKDERHPSFGVI
KDFGRLCKETYTDLRAEADLLYINATTDEKKNALFDLLCCVNAADLDVDCYDYIVDNF
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SQPYSSSRRRRQDERSCEQENVSEDNVQIIGANBEPLTRTYHSQGVTYHVHGQVNISND
DPLLSQEDDTIESVDRLLSSTRIALRRRITAQRALQ"
                                                                                                                                                                                                                                                                                                       171
                                                                                                                                                                                                                                                                                                                                                                                                231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleotide sequence and transcriptional analysis of an immediate-early gene, PE36, from Bombyx mori nuclear polyhedrosis
                                                                                                                                                                                                                                                                                                                                                                                           172 CTACGITICGIAGACTATITIACATAAATAGICTACACCGITGIATACGCICCAAATACA
                                                                                                                                                                                                                                                                                                       112 AACTITITITGCACTGCAAAAAACACGCTTTTGCACGCGGGCCCAIACAIAGIACAAACI
                                                                                                                                                                                                                                                                 1; Gaps
                                                                                                                                                                                                                 Length 129609;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus
                                                                                                                                                                                                                                                              33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124772 CTACCACGTAATGTACATTTTTGCACTGCAAAAAGT 124736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTACCACACATTGAACCTTTTTGCAGTGCAAAAAGT 268
                                                                                                                                                                                                                   Score 92.2; DB 14;
Pred. No. 1.1e-17;
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Bombyx mori nucleopolyhedrovirus
Bombyx mori nucleopolyhedrovirus
                                                                                                                                                                                                                                                              0; Mismatches
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/isolate="BmNPV-N9"
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                                                                                                                                                                          complement (5854. .6387)
xref="GI:30269988"
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Yamamoto, G. and Kobayashi, M.
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Location/Qualifiers
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Faculty of Agriculture
                                                                                                                                                                                                                 Query Match
Best Local Similarity 78.3%;
Matches 123; Conservative
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Phone:
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AUTHORS
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REFERENCE
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NELRTI OIKOORMMAEIKKEPVINFKFECSVCFETYSOOSNDTCPFLIPTTCDHGFCF
KCVIDLOSNAMNIPHSIVCCPLCNTQVKMWRSLKPNAVVTCKFYKKTOERVPAVQOYK
NIIKVLOERSVISVENDKNCDINMENQAKIVALEAELKTERNHSDQYTSENRQLTEE
NTRLNEQVQELQRQYRTLRPQRGITTVNPQIGRDDSAPAELNEFFRSLAYSTISELFIE
NRVHSIGNYVAGTSGAASSCDVNVTVNFGFEN"
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                                                                                                                                                                                                                                                                                                                                                                                                                         Score 92; DB 14;
Pred. No. 5.3e-18;
0; Mismatches 45;
                                                                                                                                   /protein_id="BAA03364.1"
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                                                                                 /codon_start=1
/product="BmPE36"
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ilarity 72.6%;
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엄 ð 요 ò 셤

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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- nucleic search, using sw model OM nucleic

May 10, 2005, 01:20:43 ; Search time 616.764 Seconds (without alignments) 5413.313 Million cell updates/sec Run on:

US-09-896-888A-1 Title: Perfect score:

1 catgatgataaacaatgtat.....tgttacagcgacacatg Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

8780412 4390206 segs, 2959870667 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N\_Geneseq\_16Dec04:\* geneseqn1980s:\* geneseqn1990s:\* Database :

geneseqn2001as:\* geneseqn2001bs:\* geneseqn2002as:\* geneseqn2002bs:\* geneseqn2003as:\* geneseqn2000s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2003ds:\* geneseqn2004as:\* geneseqn2003cs:\*

geneseqn2003bs: \*

geneseqn2004bs:\*

## SUMMARIES

1   564   100.0   564   2   AAV62487   Aav62487   O. pseudo Add46875   O. pseudo Add46876   O. pseudo Add71938   O. pseudo Add71938	Result No.	Score	* Query Match	* Query Match Length DB	DB	ΩI	Description
2 548 97.2 560 12 ADQ48575 3 546.4 97.2 2773 9 ALL61306 5 101.4 18.0 279 2 AAT13730 6 101.4 18.0 133894 2 AAT13730 7 93.4 16.6 28413 10 ADC54646 9 10.9 39.6 7.0 6289 8 ABZ10059 11 39.6 7.0 9289 10 ADE84121 13 8 6.7 6289 10 ADE84121 14 36.2 6.4 2000 8 ADA71938 15 35.4 6.3 1549 6 ABQ68715 16 35.4 6.1 855 2 AAV34232 17 34.4 6.1 855 2 AAV34232 18 34.4 6.1 855 8 ACD08103 19 34.8 6.0 1891 6 AAS18541		564	100.0	564	~	AAV62487	Aav62487 O. pseudo
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17     34.4     6.1     855     2     AAV34232     Aav34232       18     34.4     6.1     855     8     ACD08103     Acd08103       19     34     6.0     1897     4     ABL19380     Abl19380       20     33.8     6.0     1991     6     AAS16541     AaS18541	c 16	35.4	6.3	1549	9	ABQ70339	
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ACN44823 ABZ42667 AAQ97304 ACN43223	ACN44822 ABZ73951 ABZ67535 ABZ73950	ABL34242 ABQ67097 AAH30400	ABL93815 AAC37066 AAC36504 ABZ17343 ADA68882	ADA70711 ADL37609 AD172470 ADO48003 ABL18801	ABL27503 ABL27502 ABL18800
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## ALIGNMENTS

AAV62487 standard; DNA; 564 BP. (first entry) (revised) 17-OCT-2003 19-JAN-1999 AAV62487; RESULT 1 AAV62487 

O. pseudotsugata multicapsid nucleopolyhedrosis virus ie2 promoter.

Orgyia pseudotsugata; multicapsid; nucleopolyhedrosis virus; OpMNPV; Op ie2; promoter; shuttle vector; transformation; melanotransferrin; immediate early baculovirus promoter; prokaryotic; transcription; bleomycin/phleomycin-type antibiotic; insect cell; transposon; ion transport peptide hormone; ss.

Orgyia pseudotsugata; polyhedrosis virus.

WO9844141-A2

08-OCT-1998

98WO-CA000282 26-MAR-1998; 97US-0049946P. 98CA-02221819. 27-MAR-1997; 28-JAN-1998;

(UYBR-) UNIV BRITISH COLUMBIA.

Hegedus DD; Theilmann DA, Pfeifer TA, Grigliatti TA,

WPI; 1998-557129/47.

Expression vectors for transforming insect cells from disparate lines useful to express heterologous DNA, e.g. to allow study of gene expression and produce commercially important proteins.

Claim 10; Page 82; 121pp; English.

This represents a Orgyia pseudotsugata multicapsid nucleopolyhedrosis virus (OpMNPV) immediate early 2 (Op ie2) promoter sequence. The invention provides a new shuttle vector for transforming insect cells

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carly baculovirus promoter; (iii) prokaryotic princationing as, an immediate early baculovirus promoter; (iii) prokaryotic promoter sequence, and (iv) selectable marker capable of conferring resistance to a bleomycin/ belowycin-type antibiotic under transcriptional control of (ii) and (iii), in insect and prokaryotic calls respectively. The vectors can be used to stably transform (especially insect) cells with heterologous DNA, useful to allow study of gene expression and direct expression of heterologous gene products e.g. commercially important proteins. They are especially useful to allow expression of the heterologous melanotransferrins, on transport peptide hormones or biologically active melanotransferrins, ion transport peptide hormones or biologically active insectional modification of particular proteins. Shuttle vectors turnes from disparate species, allowing screening of lines for optimum post translational modification of particular proteins. Shuttle vectors further comprising DNA transposable elements defining a transposon can be used to optimise heterologous protein expression and facilitate selection of desired transformants. (Updated on 17-OCT-2003 to standardise OS
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Best Local Similarity 100.0%; Pred. No. 1.1e-172;
Matches 564; Conservative 0; Mismatches 0;
prokaryotic origin of
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ВP

ADQ48575 standard; DNA; 560

RESULT 2 ADQ48575 (first entry)

09-SEP-2004

ADQ48575;

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180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       portion of one or more viral/baculoviral genomes and further containing at least two recombination sites that do not substantially recombine with each other. One or more of the recombination sites is capable of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               undergoing recombination with a compatible recombination site in the presence of one or more proteins active in lambda recombination. The mucleic acid of the invention replicates in prokaryotic and eukaryotic cells. The mucleic acid of the invention is useful for constructing recombinant virus, generating replication-defective particles, and are useful as gene therapy vectors. The mucleic acid of the invention of one or more genes in an organism, and are useful for producing and expressing fusion polypeptides. The present DNA sequence represents the OpIE2 promoter that was used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel nucleic acid molecule comprising all or a portion of one or more viral genome and further comprising two or more recombination sites that do not substantially recombine with each other, useful as gene therapy.
                                                           replication-defective particle generation; gene expression inhibition; gene therapy vector; ds; OpIE2 promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITICALGITIGCCAACAACAAGCACCTITATACTCGGTGGCCTCCCCCACCACCACCTTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 TITICATGITIGCCAACAAGCACCITITATACTCGGIGGCCTCCCCACCACCATTITIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention comprises a nucleic acid molecule consisting of all
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Frimpong K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 560 BP; 144 A; 156 C; 116 G; 144 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                site; recombinant virus;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Madden K,
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Harwood S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Fig 16; 555pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exemplification of the invention.
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2002US-0398617P.
2002US-0427231P.
2003US-0456496P.
2003US-0474940P.
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                 promoter DNA sequence
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Best Local Similarity 100.8
Matches 548; Conservative
                                                                                                                                                                                                                                                                                                                   INVITROGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                          RP, Welch PJ,
                                                                                                                                                                                                                                                                                                                                 BENNETT R P.
WELCH P J.
HARWOOD S.
MADDEN K.
FRIMPONG K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2004-132944/13.
                                                                                                                                     WO2004009768-A2.
                                                                                                                                                                                                                                           26-JUL-2002;
19-NOV-2002;
24-MAR-2003;
03-JUN-2003;
                                             vector;
                                                                                                       Unidentified
                                                                                                                                                                                                                              18-JUL-2002;
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(FRIM/)
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(HARW/)
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Indels

Length 2773;

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124 180 184 240

244 300 304 360

364

420

424

480

484

540

544

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viral vector; recombination site; recombinant virus; replication-defective particle generation; gene expression inhibition; gene therapy vector; ds; plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                305 GGGTCCCTCTCTCACCTACGAATCACATTATCGGACCGGACGAGTGTTGTTATTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               365 GACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               425 GGACGCGCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACACGAGGGGCCCC
                                                                                                                                                 CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCCAACAACAATTCTGTTGAACTGTG
                                                                                                                                                                                 61 TITICALGITIGCCAACAAGCACCTITATACTCGGTGGCCTCCCCACCACCAACTITITI
                                                                                                                                                                                                     65 TTTTCATGTTTGCCAACAACAACCTTTATACTCGGTGGCCTCCCCACCACCAACTTTTTT
                                                                                                                                                                                                                                                            GTAGACTATTTTACATAATAGTCTACACCGTTGTATACGCTCCAAATACACTACCACAC
                                                                                                                                                                                                                                                                                                                 185 GTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACACTACCACAC
                                                                                                                                                                                                                                                                                                                                         301 GGGTCGCGTCCTGTCACGTACGAATCACATTATCGGACCGGACGAGTGTTGTCTTATCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  485 GTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAACACAGTTGAACAG
                                                                                                                                 1 CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTG
                                                                                                                                                                                                                                      gene therapy. The present sequence is p2ZOp2F expression vector for insect cells. This sequence is used to illustrate the method of the
                                                     Sequence 2773 BP; 669 A; 750 C; 673 G; 681 T; 0 U; 0 Other;
                                                                            Score 548; DB 9; Le
Pred. No. 3.8e-167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viral vector-related plasmid - pIB/V5-His-DEST.
                                                                    97.2%; Scor.
100.0%; Pred. No. ...
0; Mismatches
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                                                                                           Best Local Similaricy .....
Matches 548; Conservative
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                                                                                          Similarity
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                            invention
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                                                                               Query Match
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ADQ48539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to immunogenic analogues of multimeric proteins such as immunogenic variants of interleukin 5 (IL5) and tumour necrosis factor alpha (TRF, TNFalpha) and methods for production of immunogenic analogues. The immunogenic analogue is useful for preparing a composition for treating inflammatory diseases, e.g., arthritis. It is also used in
                                         300
                                                                                          360
                                                                                                                                             420
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                                                                                                                                                          GACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACA 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Multimeric protein; interleukin 5; IL5; TNPalpha; inflammatory disease; tumour necrosis factor alpha; gene therapy; arthritis; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New immunogenic analogue of a polymeric protein, useful for preparing composition for treating inflammatory diseases e.g. arthritis.
GGGTCGCGTCCTGTCACGTACGAATCACATTATCGGACCGGACGAGTGTTGTCTTATCGT
                                                                                                                                          GACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACA
                                                                                                                                                                                                             GGACGCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACGGGACACGAGGGGCCCC
                                                                                                                                                                                                                                                GTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAACACAGTTGAACAG
                                                                                                                  GGACGCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACACGAGGCGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Voldborg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         p2ZOp2F expression vector for insect cells.
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16-NOV-2001; 2001US-0331575P
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NIELSEN F S.
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VOLDBORG B.
                                                                                                                                                                                                                                                                                                     CATCTGTT
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(KLYS/)
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GGACGCCCCCCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACAAGGCGCCC
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                                                                                                                                                                AAT13730/c
ID AAT13730 standard; DNA; 279
                                                                                                                                                                                                                          (revised)
(first entry)
                                                                                             548
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                                                                                             CATCTGTT
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06-SEP-1996
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                                                                                                                                                                                                                                                                              The invention comprises a nucleic acid molecule consisting of all or a portion of one or more viral/baculoviral genomes and further containing at least two recombination sites that do not substantially recombine with each other. One or more of the recombination sites is capable of undergoing recombination with a compatible recombination site in the presence of one or more proteins active in lambda recombination. The nucleic acid of the invention replicates in prokaryotic cells. The nucleic acid of the invention is useful for constructing a recombinant virus, generating replication-defective particles, and are useful as gene therapy vectors. The nucleic acid of the any vectors. The nucleic acid of the invention is useful for producing and expression of one or more genes in an organism, and are useful for producing and expressing fusion polypeptides. The present DNA sequence represents a plasmid that was used in the
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                                                                                                                                                                                                           nucleic acid molecule comprising all or a portion of one or more genome and further comprising two or more recombination sites that substantially recombine with each other, useful as gene therapy.
                                                                                                                                                                 Franke KE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTAGACTATTTTACATAAATAGTCTACACCCGTTGTATACGCTCCAAATACACTACCACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTTCATGTTTGCCAACAACACCTTTATACTCGGTGGCCTCCCCACCACCAACTTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTTTCATGTTTGCCAACAAGCACCTTTATACTCGGTGGCCTCCCCACCAACTTTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGTCGCGTCCTGTCACGTACGAATCACATTATCGGACCGGACGAGTGTTGTCTTATCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5038 BP; 1342 A; 1178 C; 1198 G; 1320 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 12; Length 5038;
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                                                                                                                                                                Madden K, Frimpong K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 96.9%; Score 546.4; DB 12
Best Local Similarity 99.8%; Pred. No. 1.7e-166;
Matches 547; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                           Example 18; Page 395-403; 555pp; English.
                                                                                                                                                                 Harwood S,
                                                                                                                                                                                                                                                                                                                                                                                                                                        exemplification of the invention
           26-JUL-2002; 2002US-0398617P.
19-NOV-2002; 2002US-0427231P.
24-MAR-2003; 2003US-0466496P.
03-JUN-2003; 2003US-0474940P.
                                                                     CORP
                                                                                                                                                                Bennett RP, Welch PJ,
                                                                               BENNETT R P. WELCH P J. HARWOOD S.
                                                                                                                                                                                      WPI; 2004-132944/13.
                                                                                                                MADDEN K.
FRIMPONG K.
FRANKE K E.
                                                                     INVITROGEN
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(MADD/)
(FRIM/)
                                                                                                                                         (FRAN/)
                                                                                           WELC/)
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AAT13636-731 show open reading frames 13, 20, 22-30, 32, 38, 41-46, 50-60, 62-63, 66, 68-79, 81-87, 91-92, 96-98, 101-103, 106-127, 129-130, 140 -146, 148-150, 152 and 154 from a total of 154 ORFs identified in the Autographa californica nuclear polyhedrosis virus (AcNPV) clone 6. Each gene is numbered according to its position in the virus genome beginning that left end of the linear map, and irrespective of its orientation. The direction of transcription is relative to that of the polyhedrin gene. Of the 154 ORFs identified it was found that some of the ORFs (ORFs 77, 30, 32, 71, 86, 123, 126 and 127) are dispensable for virus replication in cell culture or insect larvae. These genes can be deleted from the genome to: (a) provide additional sites for inserting single or multiple copies of foreign genes; and (b) to reduce the size of the virus complementary strand relative to the polyhedrin gene. The present sequence is designated ORF 152, and is on the complementary strand relative to the polyhedrin gene. (Updated on 16-OCT-2003 to standardise
                                                                                                                                                                                              540
480
                                                                                                    540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Autographa californica nuclear polyhedrosis virus clone 6; disruption; non-essential gene; heterologous protein production; expression vector; baculovirus; ss.
                                                                                                                                                           GTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAACACAGTTGAACAG
                                                                                                    GTCCCGCTTATCGCCCCTATAAATACAGCCCGCAACGATCTGGTAAACACAGTTGAACAG
421 GGACGCGCCTCCATATCAGCCGCGCTTATCTCATGCACGTGACCGGACACGAGGCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Autographa californica nuclear polyhedrosis virus complete genome sequence - useful in the prodn. of vectors for enhanced heterologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .279
/*tag= a
/number= ORF 152
/note= "corresponds to AcNPV nucleotides complement
(132387-132109)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence - useful in the prodn. of vectors for enhanced heterc
protein expression, such as interleukin(s), interferon(s) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Autographa californica nucleopolyhedrovirus; clone 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNCIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACNPV ORF 152, residues 132387-132109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 90-186; 122pp; English.
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Query Match

Best Loca Matches

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AAT13635;

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Length 133894;

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132265 CTACAAATCGTAGACTATTTTATTAGAATAGTCTACACTGTACGATACGCTCCCAATATA 132265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a Bombyx mori (silk worm) polyhedrosis virus in which open reading frame 8 (ORF 8) gene is inactivated. The inactivated orfs gene is useful for suppressing movement of silkworm and efficiently prevents the movement of a silkworm from a chamber in which it is raised. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mori polyhedrosis virus in which open reading frame gene is or its variant, useful for suppressing movement of Bombyx
                                                                                                                               132384 AATTTTTTGCAATGCAAAAAAGTTCACTTTTGCCTGACACTCCATATACAGTACAATCT
                                                                                                                                                                                            172 CTACGTTCGTAGACTATTTTACATAATAGTCTACACCGTTGTATACGCTCCAAATACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22231 AATTTTTTGCAATACAAAAAGTTCGCCTATGTTTGACATATAATATACAGTACGAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       172 CTACGTTTCGTAGACTATTTTACATAATAGTCTACACCGTTGTATACGCTCCAAATACA
                                                                                               Sequence 28413 BP; 8394 A; 5713 C; 5940 G; 8366 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                      132264 chácháchácharcháchrirtricchrinachahahaghrahrirtric 132218
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                                                                                                                                                                                                                                                                                        232 CTACCACACTTGAACCTTTTTGCAGTGCAAAAAGTACGTGTCGGC 278
Score 101.4; DB 2;
Pred. No. 4.4e-21;
0; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BmNPV genomic DNA nucleotides 100001-128413.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ds; silkworm; silkworm movement supression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bombyx mori nuclear polyhedrosis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 5; SEQ ID NO 3; 53pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADC51646 standard; DNA; 28413
  18.0%;
75.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-JUL-2001; 2001JP-00209305.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-JUL-2001; 2001JP-00209305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (RIKA ) RIKAGAKU KENKYUSHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 121; Conservative
                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-516415/49.
                         Best Local Similarity
Matches 126; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel Bombyx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inactivated,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADC51646;
     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ADC51646/c
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                                                                                                                                                                                              171
                                                                                                                                                                                                                                           217
                                                                                                                                                                                                                                                                                           CTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACA 231
                                                                                                                                                                                                                                                                                                                                        CTACAAATCGTAGACTATTTTTAGAATAGTCTACACTGTACGATACGCTCCCAATATA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Autographa californica nuclear polyhedrosis virus clone 6; disruption; non-essential gene; heterologous protein production; expression vector;
                                                                                                                                                                                              AATTITITIGCAATGCAAAAAGTTCACTTTTTGCCTGACACTCCATATACAGTACAATCT
                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Autographa californica nuclear polyhedrosis virus complete genome sequence - useful in the prodn. of vectors for enhanced heterologous protein expression, such as interleukin(s), interferon(s) and
                                                                                                                                            ö,
                                                                                               DB 2; Length 279;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Cracracacrarcaacririririccarracaaaaaacrircarririricc 110
                                                                                            Score 101.4; DB 2; Length
Pred. No. 2.5e-22;
0; Mismatches 41; Indels
                                                  0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Autographa californica nucleopolyhedrovirus; clone 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Page 90-186; 122pp; English.
                                                  A; 36 C; 68 G; 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAT13635 standard; DNA; 133894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Possee R, Ayres M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94GB-00013420
                                                                                          18.0%;
Local Similarity 75.4%;
Les 126; Conservative
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACNPV genomic DNA clone 6.
                                                  BP; 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1996-087670/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  baculovirus; ss.
                                                                                                                                                                                            112 AACTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-JUL-1994;
                                                  Sequence 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUN-1995;
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03-SEP-1996
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AAT13635/C
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AC AAT1.
XX
DT 16-00
DT 03-Si
XX
DE ACNP

22172

231

22111 CTACTACTATCAACTTTTTGCATTACAAAAAGTTCATTTTTGC 22065

232 CTACCACACTTGAACCTTTTTGCAGTGCAAAAAAGTACGTGTCGGC 278

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U; 0 Other;

Sequence 133894 BP; 39195 A; 27151 C; 27347 G; 40201 T; 0

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The invention comprises a nucleic acid molecule consisting of all or a portion of one or more viral/baculoviral genomes and further containing at least two recombination sites that do not substantially recombine with each other. One or more of the recombination sites is capable of undergoing recombination with a compatible recombination of the presence of one or more proteins active in lambda recombination. The nucleic acid of the invention replicates in prokaryotic and eukaryotic cells. The nucleic acid of the invention replication defective particles, precombinant virus, generating replication-defective particles, and are useful as gene therapy vectors. The nucleic acid of the invention is useful for constructing a preventing/inhibiting the expression of one or more genes in an organism, and are useful as gene therapy vectors. The nucleic acid of the invention is also useful for producting and expressing fusion polypeptides. The present DNA sequence represents a recombination region of a plasmid that was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acid molecule comprising all or a portion of one or more viral genome and further comprising two or more recombination sites that do not substantially recombine with each other, useful as gene therapy.
                                                                                                                                                                                           viral vector; recombination site; recombinant virus; replication-defective particle generation; gene expression inhibition; gene therapy vector; ds; plasmid; recombination region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Franke KE;
                                                                                                                                                     Viral vector-related plasmid pIB/V5-His-DEST recombination region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Madden K, Frimpong K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 141 BP; 43 A; 36 C; 27 G; 34 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.0%; Score 62; DB 12;
100.0%; Pred. No. 1.2e-09
:ive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Harwood S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 17; 555pp; English
                                         ADQ48576 standard; DNA; 141 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                     18-JUL-2002; 2002US-0396335P.
26-JUL-2002; 2002US-0398617P.
19-NOV-2002; 2002US-0427231P.
24-MAR-2003; 2003US-0456496P.
03-JUN-2003; 2003US-0456496P.
                                                                                                                                                                                                                                                                                                                                                                                  18-JUL-2003; 2003WO-US022437
                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INVITROGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Welch PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BENN/) BENNETT R P.
(WELC/) WELCH P J.
(HARW) HARMOOD S.
(MADD/) MADDEN K.
(FRIM/) FRIMFONG K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-132944/13.
                                                                                                                                                                                                                                                                                                           WO2004009768-A2.
                                                                                                                                                                                                                                                                    Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bennett RP,
                                                                                                                  09-SEP-2004
                                                                                                                                                                                                                                                                                                                                               29-JAN-2004
                                                                              ADQ48576;
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RESULT 8
                       ADQ48576
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The present invention describes a method for detecting and differentiating between haematopoietic cell proliferative disorders associated with at least 1 gene and/or their regularcory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118 represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used: invention oligonucleotides from the present invention can be used: invention oligonucleotides from the present invention acide used: for differentiating between healthy haematopoietic cells and proliferative lymphocytic leukaemia and acute myelogenous leukaemia, as probes for determining the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder related DNA amplification of haematopoietic cell proliferation disorder related buna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          enables a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pelet C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferative disorders. The present method enables highly specific classification of haematopoietic cell proliferative
                                                                                                                                                                                                                                                  Haematopoietic cell proliferation disorder related DNA sequence #199.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorders allowing for improved and informed treatment of patients
                                                                                                                                                                                                                                                                                     Human; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Howe A, Mueller J;
G, Lesche R, Leu E;
Mueller V, Otto T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6289 BP; 1680 A; 178 C; 1488 G; 2943 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Guetig D,
P, Grabs
Model F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 28; SEQ ID NO 199; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Berlin K, Braun A, Distler J,
Olek A, Piepenbrock C, Adorjan
Lewin A, Lipscher E, Maier S,
                                                                                                                          ABZ10059 standard; DNA; 6289 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAR-2002; 2002WO-EP003401.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-MAR-2001; 2001US-0278333P.
                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lipscher E, N
, Ziebarth H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (EPIG-) EPIGENOMICS AG
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                     62
                                                                                                                                                                                                                                                                                                                                                                                                                  WO200277272-A2
                                                                                                                                                                                                          16-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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Schwope I,
                                                                                                                                                                 ABZ10059;
                     61
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DB 8; Length 6289;

Score 39.6;

7.0%;

9

487 CTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAACACAGTTGAACAGCATCTG CTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAACACAGTTGAACAGCATCTG

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Gaps

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0; Indels

62; Conservative

547 TT 548

d 8

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Local Similarity

Best Loca Matches

1.2e-09;

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The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with baseling to genes associated with fumour suppression and concequence having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (Ss) and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation state and/or single cutleotide polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be compared to another set of partients and/or epigenetic parameters which are disadvantageous to patients. The present sequence is one of the 533 genomic sequences derived from tumour suppressor genes and oncogenes. Note: The sequence data for this patent did not form part of the printed specification, but two ont thybublished_pot_esquences
4896 AATTTATTTATATAACCAAATAAAACTATTATAAATCCACTACCAAATATCATTCAAAAA 4837
                                                                                                      4836 TAATAATTTTTAAAACATTATTTATAAAAATGGTCACAATTCTTTTTACTCAAAAAATA 4777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fragments of chemically modified genes associated with tumor suppressor genes and oncogenes, useful in designing primers and probes for analyzing diseases associated with cytosine methylation state e.g. cancer.
                                                               231
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP; cytosine methylation; ds.
                                                               172 CTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACA
                                                                                                                                                                                                                                                                                                                                                                                                             Tumour suppressor gene derived chemically modified sequence #223
                                                                                                                                                                                    4776 ATACAACTTTCCTCTCCTATAAAACGAAAAAAAAA 4739
                                                                                                                                              232 CTACCACACTTGAACCTTTTTGCAGTGCAAAAAGTA 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 223; 27pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Berlin K;
                                                                                                                                                                                                                                                                                           AAS46501 standard; DNA; 9289 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-APR-2000; 2000DE-01019058.
07-APR-2000; 2000DE-01019173.
30-JUN-2000; 2000DE-01033529.
01-SEP-2000; 2000DE-01043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-MAR-2001; 2001WO-EP002955
                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-602752/68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200168912-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a method of detecting and differentiating between lymphoid cell proliferative disorders associated with at least one gene and/or their regulatory regions in a subject by contacting a target nucleic acid in a biological sample obtained from the subject with at least one reagent or series of reagents that distinguish between methylated and non-methylated CpG dinucleotides within the target nucleic acid. The genes and/or their regulatory regions are preferably selected from MDR1, CSMK2B, EGR4, AR, CDK4, RB2, CDC25A, GPIb beta, MYOD1, CDH3, MYCL1, ELK1, ABL1, APC, BCL2, CDH1, CDKN1A, CDKN1B, CDKN2B, FOS, GSK7P1, HIC-1, MGMT, MLH1, MOS, MYC, PTEN, RBL2, TGFBR2, TP73, CDKN1C, GSK3beta, ESR1, APAF1, BAK1, BAX or HOXAS. Oligomers, peptide nucleic acid (PNA)-oligomers and/or isolated nucleic acids based on the sequences of the genes are useful for detecting the methylation state of all the
                                                                                                                                                                                                                                1836 TAATAATTITITAAAACATTATTATAAAAATCGTCACAATTCTTTTTACTCAAAAAATA 7777
                                                                                                                        231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          one
                                                                                                                                                                                           172 CTACGTTTCGTAGACTATTTTACATAATAGTCTACACCGTTGTATACGCTCCAAATACA
                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      disorders comprises contacting a target nucleic acid with at least or reagent that distinguishes between methylated and non-methylated CpG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detecting and differentiating between lymphoid cell proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nimmrich I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human lymphoid cell proliferative disorder gene derived DNA #57
                                                                                     ó,
                0 U; 0 Other;
                                                   Length 9289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ds; lymphoid cell proliferative disorder; methylation; methylated CpG dinucleotide; single nucleotide polymorphism; diffuse large B-cell lymphoma; mantle cell lymphoma; chronic lymphocytic leukemia; small lymphocytic lymphoma;
                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maier S,
                                                                                                                                                                                                                                                                                                    7776 ATACAACTTTCCTCTCCTATAAAACGAAAAAAAATA 7739
                                                                                 74;
                Sequence 9289 BP; 2515 A; 206 C; 2097 G; 4471 T;
                                                   DB 4;
                                                                                                                                                                                                                                                                 232 CTACCACACTTGAACCTTTTTGCAGTGCAAAAAGTA
                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Becker E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             follicular lymphoma; diagnosis; prognosis.
                                                  Score 39.6;
Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                             BP
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28-DEC-2001; 2001DE-01064501.
                                                                                                                                                                                                                                                                                                                                                                                             ADE84121 standard; DNA; 9289
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                                                  7.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                     84; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-457621/43.
                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003044226-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dinucleotides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Burger M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                 ADE84121;
                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                          RESULT 11
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Wed May 11

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CpG dinucleotides within one or more the sequences, or their complements, for determining the cytosine methylation state and or single nucleotide polymorphisms (SNPs), and for differentiating at least two of the medical conditions such as diffuse large B-cell lymphoma, mantle cell lymphoma, chronic lymphocytic leukemia, small lymphocytic lymphoma and follicular chronic lymphocytic leukemia, small lymphocytic lymphoma and follicular differentiation between subclasses, diagnosis, prognosis, treating and/or monitoring of lymphoid cell proliferative disorder. This sequence represents a nucleic acid of a pretreated genomic DNA derived from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7836 TAATAATITTTAAAACATTATTATAAAAATCGTCACAATTCTTTTTACTCAAAAATA 7777
                                                                                                                                                                                                                                                                                                                                                                                                  231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172 CTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACA
                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                           Sequence 9289 BP; 2515 A; 206 C; 2097 G; 4471 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                Length 9289;
                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     232 CTACCACACTTGAACCTTTTTGCAGTGCAAAAAGTA 269
                                                                                                                                                                                                                                                                                                           Score 39.6; DB 10;
Pred. No. 0.16;
0; Mismatches 74;
                                                                                                                                                                                                                                                                                                              7.0%;
                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 53.2°
Matches 84, Conservative
                                                                                                                                                                                                                       above mentioned genes.
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Haematopoietic cell proliferation disorder related DNA seguence #345.
                                                           Human; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; gene; ds.
            ABZ10205 standard; DNA; 6289 BP
                                   (first entry)
                                   16-JAN-2003
                        ABZ10205;
                                                                                   Ношо
     RESULT 12
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Howe A, Mueller J; G, Lesche R, Leu E; Mueller V, Otto T, Guetig D, P, Grabs C Model F, N 26-MAR-2002; 2002WO-EP003401. 26-MAR-2001; 2001US-0278333P. (EPIG-) EPIGENOMICS AG WO200277272-A2. 03-OCT-2002.

Berlin K, Braun A, Distler J, Olek A, Piepenbrock C, Adorjan Lewin A, Lipscher E, Maier S, Ziebarth H; Schwope I,

WPI; 2003-018942/01.

Pelet C;

Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides.

Claim 28; SEQ ID NO 345; 117pp; English.

differentiating between haematopoietic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in subject. The method comprises contacting a target nucleic acid in a present invention describes a method for detecting and

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dinucleotides within the target nucleic acid. Ma209861 to ABZ1118
represent specifically claimed nucleotide sequences from the present
invention. Oligonucleotides from the present invention can be used:
invention. Oligonucleotides from the present invention can be used:
differentiating between healthy haematopoietic cells and proliferative
disorder haematopoietic cells; for differentiating between acute
lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
configuration the cytosine methylation state and/or single nucleotide
polymorphisms (SNPs) of haematopoietic cell proliferation disorder
related sequences and their complements; and as primers for the
muplification of haematopoietic cell proliferation disorder related DNA
sequences. The nucleotide sequences from the present invention can also
be used for detecting a predisposition to, differentiation between
cube used for detecting a predisposition to, differentiation between
the used adaposis, prognosis, treatment and/or monitoring of
haematopoietic cell proliferative disorders. The present method enables a
highly specific classification of haematopoietic cell proliferative
disorders allowing for improved and informed treatment of patients
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4896 ААТТТАТТТАТАТАБАССАААТААААСТАТТАТААТССАСТАССАААТАТСАТТСААААА 4837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4836 TAATAATTITTAAAACATTATTATAAAAATCATCACAATTCTTTTTACTCAAAAATA 4777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Detecting and differentiating between lymphoid cell proliferative disorders comprises contacting a target nucleic acid with at least one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 CTACGTTTCGTAGACTATTTTACATAATAGTCTACACCGTTGTATACGCTCCAAATACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
    ological sample obtained from the subject with at least 1 reagent,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ds, lymphoid cell proliferative disorder; methylation; methylated CpG dinncleotide; single nucleotide polymorphism; SNP; diffuse large B-cell lymphoma; mantle cell lymphoma; chronic lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human lymphoid cell proliferative disorder gene derived DNA #133
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                      distinguishes between methylated and non-methylated CpG
                                                                                                                                                                                                                                                                                                                                                                     Sequence 6289 BP; 1680 A; 0 C; 1488 G; 3121 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                            Length 6289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4776 ATACAACTTTCCTCTCCCTATAAAAAAAAAAAAAA 4739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232 CTACCACACTTGAACCTTTTTGCAGTGCAAAAAGTA
                                                                                                                                                                                                                                                                                                                                                                                                            DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                              0.45;
                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 38; DB 8
; Pred. No. 0.45;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               follicular lymphoma; diagnosis; prognosis.
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                                                                                                                                                                                                                                                                                                                                                                                                          6.7%;
52.5%;
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28-DEC-2001; 2001DE-01064501
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hes 83; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-457621/43.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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ADE84197/c
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from MDR1, CSNKZB, EGR4, AR, CDK4, RB2, CDC25A, GPIb beta, WYOD1, CDH3, MYCL1, BELK1, ABL1, ARC, BCL1, CDH1, CDKN1A, CDKN1B, CDKN2B, FOS, MYCL1, ELK1, ABL1, ABL1, MOS, MYC, PTEN, RBL2, TGFBR2, TP73, CDKNIC, GSK3beta, ESR1, APAF1, BAK1, BAX or HOXAS. Oligomers, peptide nucleic acid (PNA)-oligomers and/or isolated nucleic acids based on the sequences of the genes are useful for detecting the methylation state of all the CpG dinucleotides within one or more the sequences, or their complements, for determining the cytosine methylation state and or single nucleotide polymorphisms (SNPS), and for differentiating at least two of the medical conditions such as diffuse large B-Cell lymphoma, mantle cell lymphoma, chronic lymphocytic leukemia, small lymphocytic lymphoma and follicular lymphoma. They are also useful for detecting of a predisposition to, insphenent subclasses, diagnosis, prognosis, treating and/or represents a nucleic acid of a pretreated genomic DNA derived from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7896 AATTTATTTATATATAAACGAAATAAAACTATTATAAATCCACTACCAAATATGATTCAAAAA 7837
                                                                                         The invention relates to a method of detecting and differentiating between lymphoid cell proliferative disorders associated with at least one gene and/or their regulatory regions in a subject by contacting a target nucleic acid in a biological sample obtained from the subject with at least one reagent or series of reagents that distinguish between methylated and non-methylated CDG dinucleotides within the target nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 CTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant, bacterial infection; fungal infection; viral infection; rice; gene; ds.
reagent that distinguishes between methylated and non-methylated CpG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9289 BP; 2515 A; 0 C; 2097 G; 4677 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 38; DB 10; Length 92
Pred. No. 0.54;
0; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7776 aracaactrrccrcrccraraaaacaaaaaaaaaa 7739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                232 CTACCACACATTGAACCTTTTTGCAGTGCAAAAAGTA 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10;
                                                        Claim 26; SEQ ID NO 193; 448pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADA71938 standard; DNA; 2000 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-JUN-2001; 2001WO-IB001105
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Best Local Similarity 52.5
Matches 83; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  above mentioned genes.
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                    dinucleotides.
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The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  313 RYATCYWCCCYRKGWYSRRSMMRTAGKWKWRGRSWSWSKWYKWYKKGWKKSYYMSYG 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  253 WARSSGTWSRSAAKRTYKGYSTSRRAKMMRACRMYSACRRYSRTSYYGGCSYGGSKWKY 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 MSKSCSMRMTCSSWCSCCYTCYYGAMCWSCCMSMMYMGSCGCYTRGWKWRSKYSMCCKKY 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 CTGCAAAAAACACGCTTTTGCACGCGGGCCCATACATAGTACAAACTCTACGTTTCGTA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74
                                                                                      Identifying at least one gene involved in plant resistance or response to pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 GACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACACTACCACATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       310 AKYWKYWYKRRGIMSWYGKSYKKKYC--IWWCYMKCMRCYRWRKMMRKKTKYSKRCYCW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             304 TCGCGTCCTGTCACGTACGAATCACATTATCGGACCGGACGAGTGTTGTCTTATCGTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 CSCCTKYCSYTGYYRYCKWYKYSYYKCYYCYWYMSYMRKMKCMCSRSCSSWMSCAYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGCGCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACGAGGCGCCCGTC
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                Zon
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                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;
 Hon
Goff SA, Hor
Z, Zhu T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 11.3%; Pred. No. 1;
Matches 42; Conservative 169; Mismatches 157;
 Glazebrook J, Goff
Whitham S, Xie Z,
                                                                                                                                                                                Claim 27; SEQ ID NO 5263; 899pp; English.
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Tao Y,
   Cooper
                                                                                                                                                                                                                                                                                                                                                                               illustrate the invention.
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                Quan S,
                                                    WPI; 2003-175290/17.
 Chen W,
                                                                                                                                              gene expression.
 Chang H, Che
Katagiri F,
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ABOT1212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to pathogenicity of Listeria (potential therappeutic agents), also for treating infections by Listeria, and are useful as immunogens in anti-Listeria vaccines. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp. wibo.int/pub/published_pot_sequences. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                         New genomic sequences from Listeria species, useful for detection, treatment and prevention of infection, also related polypeptides, antibodies and modulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention relates to nucleic acid sequences (ABQ67188-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 6.3%; Score 35.4; DB 6; Length 986; Best Local Similarity 56.4%; Pred. No. 1.3; Matches 66; Conservative 0; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 986 BP; 295 A; 199 C; 157 G; 328 T; 0 U; 7 Other;
                                                                                                                                                                                                                                                                                                                                                                                                       Claim 14; SEQ ID NO 1528; 180pp; French.
                                                                                                                                                                            (INSP ) INST PASTEUR.
(CNRS ) CNRS CENT NAT RECH SCI.
                                                                                                04-OCT-2001; 2001WO-FR003061
                                                                                                                                        04-OCT-2000; 2000FR-00012697
                                                                                                                                                                                                                                         Kunst F, Glaser P;
                                                                                                                                                                                                                                                                                 WPI; 2002-332479/37
                  WO200228891-A2.
                                                        11-APR-2002.
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Search completed: May 10, 2005, 04:32:40 Job time : 623.764 secs

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366 GACGCCCAGCTTCCTGTGTTGCTAACCGCAGCCGAACGCAACTCCTTATCGGAACAGGACG 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 SRYRCHMSGKWCYSCCGYCCSACRMCYCWTRRMKSWYSSRKSRMCCRYMSMSSAYRYSSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 RKMYYWWKYWWKSWWCYRMGAAMYGMSARAYRMYASMSACKMCSRMMKMWRCWR
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Sequence 89, Appl
Sequence 1, Appli
Sequence 25113, A
                                                                              May 10, 2005, 04:19:16 ; Search time 187.525 Seconds (without alignments) 4921.273 Million cell updates/sec
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Sequence 1628, 2
Sequence 12642, 3
Sequence 1303, 3
Sequence 6433, A
Sequence 6433, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 103819,
Sequence 103820,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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(cgn2_6/ptodata/1/ina/5A_COMB.seq:*

//cgn2_6/ptodata/1/ina/5B_COMB.seq:*

//cgn2_6/ptodata/1/ina/6A_COMB.seq:*

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//cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*

//cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-148-545-89

US-08-270-767-25113

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US-09-249-016-103819

US-09-949-016-103821

US-09-949-016-103863

US-09-949-016-103865

US-09-949-016-103865

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US-09-949-016-160231

US-09-949-016-160231

US-09-949-016-160274

US-09-949-016-160275

US-09-949-016-160276

US-09-949-016-16228

US-09-949-016-16233

US-09-949-016-13505

US-09-949-016-13505
                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                      nucleic search, using sw model
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137, 1220			Gaps	CGTAGA  :: CGWKSK	CATTGA : : ARRSMM	CGGGTC:	FGACAG ::: SMKYRR
acuente educace educac			. 6	STTT(  :::	CACA( ::: SMYG;	TTATO SYSCI	ATCG: :: rgsr(
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TITLE OF INVENTION: 70 Human Secreted Proteins
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APPLICATION NUMBER: PCT/US98/04482
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APPLICATION NUMBER: 60/040,333
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APPLICATION NUMBER: 60/047,587
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                            Sequence 89, Application US/09148545
Patent No. 6590075
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60/056,662

60/056,880

60/043,312

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2939 AAATAATGTTTGGTGGAAATGTTCATTAAACATCATTACAAATTTAATGAAAAAGCATGC 2880
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 TIGCCAACAAGCACCTITATACTCGGTGGCCTCCCCACCACCAACTTTTTGCACTGCAA 129
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                                                                                                                                                                                                        NUCLEIC ACIDS,
AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/693,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION 536
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 17-FEB-1994
PRIOR APPLICATION BATA:
APPLICATION NUMBER: WO PCT/FR95/00172
FILING DATE: 14-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: 38,619
REFERENCE/DOCKET NUMBER: ST94008-US
TELECOMMUNICATION INFORMATION:
                                                                    GENERAL INFORMATION:
APPLICANT: HABERT-CRIOLI, Estelle
APPLICANT: AMIRANOFF, Brigitte
APPLICANT: LOQUET, Isabelle
ITILE OF INVENTION: GALANIN RECEPTOR, NUC
ITILE OF INVENTION: TRANSFORMED CELLS AND
ITILE OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Rd. 3C43
             Sequence 1, Application US/08693308 Patent No. 6447996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPAONE: (610)454-3839
TELEFAX: (610)454-3808
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3083 base pairs
TYPE: nucleic acid
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FEATURE:
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787..1836
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Best Local Similarity
Matches 68; Conserva
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EARLIER APPLICATION NUMBER: 60/047,593
EARLIER APPLICATION NUMBER: 60/047,614
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER PILING DATE: 1997-06-23
EARLIER FILING DATE: 1997-04-11
EARLIER FILING DATE: 1997-04-11
EARLIER FILING DATE: 1997-04-11
EARLIER PILING DATE: 1997-04-11
EARLIER APPLICATION NUMBER: 60/043,576
EARLIER PILING DATE: 1997-04-11
EARLIER PILING DATE: 1997-04-11
EARLIER PILING DATE: 1997-04-11
EARLIER PILING DATE: 1997-06-22
EARLIER FILING DATE: 1997-08-22
EARLIER PILING DATE: 1997-08-22
EARLIER PILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,891
EARLIER PILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER PILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER PILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-0
R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/057,761

R APPLICATION NUMBER: 60/047,599

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,588

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,588
                                                                                                                                                                                                                                                           R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,586

R APLING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,590

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,594

R APPLICATION NUMBER: 60/047,594

R APPLICATION NUMBER: 60/047,594

R APPLICATION NUMBER: 60/047,589
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TYPE: DNA
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: MITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1212 TAACTCGATGTAGCATCTCCAGATACAATTGAGCTCATAGAACTGTTTGAAAGGGAAAAT 1153
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Patent No. 6703491

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REPERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9827
LENGTH: 5003
                                                                       GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Nucleic 7326-094
FILE REFERENCE: FILE REFERENCE: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 25113
LENGTH: 902
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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US-09-270-767-25113/c
; Sequence 25113, Application US/09270767
; Patent No. 6703491
                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Drosophila melanogaster
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Best Local Similarity 56.4%;
Matches 62; Conservative
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GENERAL INFORMATION:
GURRENT FILIAGE DATE:
GOVERAL GOVERN:
FRIOR APPLICATION NUMBER:
GOV231,768
FRIOR PAPLICATION NUMBER:
GOV231,498
FRIOR FILIAGE DATE:
GOVERN:
FRIOR PELING DATE:
GOVERN:
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; Sequence 103821.
; Sequence 103821.
; Patent No. 681233
; GENERAL INFORMATION:
; APPLICANT: UNFURE, J. Craig et al.
; ITLE OF INVENTION: POLYWORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 601;
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Pred. No. 1.4;
0; Mismatches
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 103819
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; Sequence 103820, Application US/09949016
; Patent No. 6812339
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Best Local Similarity 56.07
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Best Local Similarity
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US-09-949-016-103820
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US-09-949-016-103865
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US-09-949-016-103864
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Sequence 103863, Application US/09949016

Patent No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REFERENCE: CLOOL 307

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-0-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PRESECTED NOS: 207012

SOFTWARE: PRESECTED WINDOWS Version 4.0
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56.0%; Pred. No. 1.4;
tive 0; Mismatches 48; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 5.7%; Score 32.2; DB 4; Length 601; Best Local Similarity 56.0%; Pred. No. 1.4; Matches 61; Conservative 0; Mismatches 48; Indels
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: F88ESEQ for Windows Version 4.0
SEQ ID NO 103821
LENGTH: 601
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US-09-949-016-103864
; Sequence 103864
; Parent No. 6812339
; GENERAL INFORMATION:
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Best Local Similarity
Matches 61; Conserva
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US-09-949-016-103821
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ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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Sequence 103865, Application US/09949016

Sequence 103865, Application US/09949016

Batent No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REFERENCE: CLOOL1307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-0

PRIOR PLING DATE: 2000-10-0

PRIOR PLING DATE: 2000-10-0

PRIOR PLING DATE: 2000-10-0

SROID NOS: 207012

SOFTWARE: FREATENCH WINDER: 60/231,498

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FREATENCH WINDER: 1000-10-00

SEQ ID NO 103865

LENGTH: 601

THE OF INVENTION OF THE O
APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTUM RE: FaetSEQ for Windows Version 4.0

LENGTH: 601

LENGTH: 601
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Best Local Similarity 56.0%;
Matches 61; Conservative
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Best Local Similarity 56.0°
Matches 61; Conservative
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RESULT 12 US-09-949-016-160230

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Sequence 160274, Application US/09949016

Patent No. 6812339
GENERAL INPOWARTION:
TEREST TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: C1001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR FILING DATE: 2000-10-20
PRIOR PLING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NOS: 207012
SEQ ID NO 160274
                                                                                    Sequence 160232, Application US/09949016
Fatent No. 681233
Fatent No. 681233
Fatent No. 681233
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: 40/09/949,016
CURRENT FILING DATE: 2000-10-20
FRIOR FILING DATE: 2000-10-20
FRIOR FILING DATE: 2000-10-03
FRIOR PRILING DATE: 2000-10-03
FRIOR PRILING DATE: 2000-10-03
FRIOR PRILING DATE: 2000-10-03
FRIOR PILING DATE: 2000-00-08
NUMBER OF SEQ ID NOS: 207012
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Pred. No. 1.4;
0; Mismatches
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Pred. No. 1.4;
0; Mismatches
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Best Local Similarity
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Best Local Similarity
Matches 61; Conserv
                                                                    JS-09-949-016-160232
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; ORGANISM: Human
US-09-949-016-160274
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ORGANISM: Human
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                     GENERAL INFORMATION:

APPLICANT: VENTER,

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPRENENCE: CLOLO1307

CURRENT APPLICATION NUMBER: 00/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

FRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SSOTHARE: FASTESEQ for Windows Version 4.0

LENGTH: 601
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Fatent No. 6812339
GENERAL INFORMATION:
FATELICATION OF 681239
FATELICATION OF 681239
FILE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
FRIOR FILING DATE: 2000-10-20
FRIOR PELICATION NUMBER: 60/241,755
FRIOR PELICATION NUMBER: 60/231,498
FRIOR PELING DATE: 2000-10-03
FRIOR PELING DATE: 2000-10-03
FRIOR PELING DATE: 2000-10-03
FRIOR PELING DATE: 2000-10-03
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Sequence 160230, Application US/09949016
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Best Local Similarity 56.0
Matches 61; Conservative
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Best Local Similarity 56.03
Matches 61; Conservative
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ORGANISM: Human
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LENGTH: 601
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523 TCTATCAGAATATGCTCTTTTTAATCCATTGGTTCCCCATCTCAGATT 571

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Search completed: May 10, 2005, 07:29:33 Job time : 189.525 secs

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Sequence 345, App Sequence 1528, Ap Sequence 3152, Ap Sequence 89, Appl Sequence 89, Appl Sequence 89, Appl

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Sequence 1463, Ap Sequence 125, App Sequence 125, App Sequence 2215, App Sequence 2215, App Sequence 5148, App Sequence 5148, App Sequence 11499, App Sequence 11499, App Sequence 11, Appl Sequence 312, App Sequence 2538, App Sequence 1, Appli

Title: Perfect score:

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100.0%; Score 564; DB 9; Length 564;
Best Local Similarity 100.0%; Pred. No. 2.4e-175;
Matches 564; Conservative 0; Mismatches 0; Indels
5.4 6.3 986 17 US-1.

5.4 6.3 986 17 US-10.

5.4 6.3 1549 17 US-10.

4 6.1 855 10 US-09-96

6 0 3056 15 US-10-25

6.0 3058 16 US-10-166-

6.0 3058 16 US-10-166-

6.0 3059 18 US-10-187-9

5.9 14429 15 US-10-37-9

7.8 2000 9 US-09-938-842A-

8 2000 1 US-09-938-842A-

8 2000 1 US-09-938-842A-

9 469 18 US-10-435-11

495 10 US-09-938-842A-

9 469 10 US-09-938-842A-

9 469 10 US-09-938-842A-

9 10 US-09-938-844-

10 US-10-425-115-1

11 US-10-186-761-1

12 US-10-186-761-1

13 US-10-186-761-1

14 US-10-186-761-1

18 US-10-186-761-1

18 US-10-186-715-55004

7 US-10-424-599-101900
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Sequence 1, Application US/0989688BA

Patent No. US20020116723A1

GENERAL INFORMATION:

APPLICANT: The University of British Columbia

TITLE OF INVENTION: Insect Expression Vectors

FILE REFERENCE: 80021-44

CURRENT APPLICATION NUMBER: US/09/896,88BA

CURRENT APPLICATION NUMBER: US/09/048,911

PRIOR APPLICATION NUMBER: 05/09/048,911

PRIOR FILING DATE: 1998-03-26

PRIOR FILING DATE: 1997-03-27

NUMBER OF SEQ ID NOS: 50

SEQ ID NO 1

LENGTH: 564
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; ORGANISM: Orgyia pseudotsugata
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Sequence 149, App
Sequence 16, Appl
Sequence 15, Appl
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Sequence 126, App
Sequence 60, Appl
Sequence 89, Appl
Sequence 89, Appl
Sequence 14, Appl
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                                                                                                                                             May 10, 2005, 05:52:55 ; Search time 1593.6 Seconds (without alignments) 2164.037 Million cell updates/sec
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/ cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
/ cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
/ cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
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                                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Sequence 38274, A Sequence 55004, A Sequence 101900,

Sequence 1, Appl: Sequence 11349, A Sequence 30372, A

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LOCATION: (561)...(566)
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NAME/KEY: misc_recomb
LOCATION: (573)...(578)
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LOCATION: (586)...(591)
OTHER INFORMATION: ECORI site
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GTAGACTATTTTACATAAATAGTCTACACGTTGTATACGCTCCAAATACACTACCACAC
                                                                            181 GTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACACTACGACA
                                                                                                               GGGTCGCGTCCTGTCACGTACGAATCACATTATCGGACCGGACGAGTGTTGTCTTATCGT
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APPLICANT: Madden, Knut
APPLICANT: Primpond, Kenneth
APPLICANT: Primpond, Kenneth
APPLICANT: Frimpond, Kenneth
APPLICANT: Frimpond, Kenneth
APPLICANT: Frimpond, Kenneth
APPLICANT: Frimpond, Kenneth
FILE REPERENCE: 0942.5450007-088
CURRENT APPLICATION NUMBER: US/10/622,088
CURRENT APPLICATION NUMBER: US/10/803/22437
PRIOR APPLICATION NUMBER: US 60/396,335
PRIOR PILING DATE: 2002-07-18
PRIOR PILING DATE: 2002-11-19
PRIOR PILING DATE: 2002-11-19
PRIOR PILING DATE: 2003-03-24
PRIOR PILING DATE: 2003-03-24
PRIOR PILING DATE: 2003-03-04-05
PRIOR PILING DATE: 2003-03-04-05
PRIOR PILING DATE: 2003-03-04-05
PRIOR PILING DATE: 2003-03-04-05
PRIOR PILING DATE: 2003-03-04-04
PRIOR PILING DATE: 2003-03-04-04
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Sequence 126, Application US/10622088
Publication No. US20040219516A1
GENERAL INFORMATION:
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SOFTWARE: Patentin version 3.2
SEQ ID NO 126
LENGTH: 560
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ORGANISM: Unknown
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Matches 548;
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CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTG
                                                                            65 TITICATGTTTGCCAACAAGCACCTTTATACTCGGTGGCCTCCCCACCACCAACTTTTTT
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Publication No. US20030185845A1
GENERAL INFORMATION:
APPLICANT: Pharmers A/S
TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
FILE REFERENCE: P1013DK00
CURRENT APPLICATION NUMBER: US/10/295,074
CURRENT FILING DATE: 2002-11-15
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin version 3.1
SEQ ID NO 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: p2ZOp2F expression vector for insect cells FEATURE:
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481 GICCCGCTTATCGCCCCTATAAATACAGCCCGCAACGATCTGGTAAACACAGTTGAACAG 540
                              485 GTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAACACAGTTGAACAG 544
                                                                                                                                                                                              US-10-846-911-60

| Sequence 60, Application US/10846911
| Publication No. US20040258660A1
| GENERAL INFORMATION:
| APPLICANT: KIYSER, Steen
| APPLICANT: RIYSER, Steen
| APPLICANT: WILLSEN, Finn Stausholm
| APPLICANT: WOURDINGS, Boren
| TITLE OF INVENTION: NOVEL IMMUNGENIC MIMETICS OF MULTIMER PROTEINS
| FILE REFERENCE: 674542-2018
| CURRENT APPLICATION NUMBER: PC/DK02/00764
| PRIOR FILING DATE: 2004-05-14
| PRIOR FILING DATE: 2001-11-16
| PRIOR FILING DATE: 2001-11-16
| PRIOR FILING DATE: 2001-11-16
| NUMBER OF SEQ ID NOS: 60
| SOFTWARE: Patentin version 3.1
| LENGTH: 2773
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NAME/KEY: misc_recomb
LOCATION: (561)..(566)
OTHER INFORMATION: HindIII site
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LOCATION: (593)..(598)
OTHER INFORMATION: BamHI site
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LOCATION: (5867..(591)
OTHER INFORMATION: ECORI site
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NAME/KEY: misc_recomb
LOCATION: (1155)..(1161)
OTHER_INFORMATION: Apall site
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LOCATION: (2128)..(2133)
OTHER INFORMATION: PetI site
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LOCATION: (625)..(630)
OTHER INFORMATION: ClaI site
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LOCATION: (2204)..(2209)
OTHER INFORMATION: NGOI site
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OTHER INFORMATION: Aval site
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LOCATION: (629)..(634)
OTHER INFORMATION: ClaI site
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LOCATION: (573)..(578
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LOCATION: (2294)..(2299)
OTHER INFORMATION: Aval, Smal, and Xmal site
NAME/KEY: misc_recomb
LOCATION: (593)..(598)
OTHER INFORMATION: BamHI site
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LOCATION: (1156)..(1161)
OTHER INFORMATION: Apall site
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LOCATION: (2551)..(2556)
// OTHER INFORMATION: Apall site
US-10-295-074-60
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NAME/KEY: misc_recomb
LOCATION: (629)..(634)
OTHER_INFORMATION: ClaI site
                                                                                       NAME/KEY: misc recomb
LOCATION: (625)..(630)
OTHER INFORMATION: Clal site
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NAME/KEY: misc_recomb
LOCATION: (2204)..(2209)
JTHER INFORMATION: Ncol site
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LOCATION: (2284)..(2289)
OTHER INFORMATION: Aval site
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LOCATION: (2128)..(2133)
DTHER INFORMATION: PstI site
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US-10-622-088-89
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Publication No. US20040219516A1
GENERAL INFORMATION:
APPLICANT: Bennett, Robert P.
APPLICANT: Harwood, Steven
APPLICANT: Frimpon, Knut
APPLICANT: Frimpon, Knut
APPLICANT: Frimpon, Venneth
APPLICANT: Frimpon, Venneth
APPLICANT: Frimpon; Steven
APPLICANT: Steven
AP
                                                                                                                                                                                                                                                                                      Length 2773;
                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                    Query Match 97.2%; Score 548; DB 18; Best Local Similarity 100.0%; Pred. No. 1e-169; Matches 548; Conservative 0; Mismatches 0;
                                                            FEATURE:
NAME/KEY: misc_recomb
LOCATION: (2294)..(2299)
OTHER INFORMATION: Aval, Smal, and Xmal site
                                                                                                                                                  FEATURE:
NAME/KEY: misc recomb
LOCATION: (2551)..(2556)
COTHER INCRATION: Apal site
US-10-846-911-60
NAME/KEY: misc recomb
LOCATION: (2284)..(2289)
OTHER INFORMATION: Aval site
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US-10-622-088-89
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181 GTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACACTACCACAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 TITICATGITTGCCAACAAGCACCTTTATACTCGGTGGCCTCCCCACCACCAACTTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 GACAGGACGCCAGCTTCCTGTGGTAACCGCAGCCGGACGCAACTCCTTATCGGAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACAGGACGCCAGCTTCCTGTTGCTAACCGCAGCGGACGCAAACTCCTTATCGGAAACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96.9%; Score 546.4; DB 18; Length 5038; 99.8%; Pred. No. 4.7e-169; cive 0; Mismatches 1; Indels 0;
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: PCT/US03/22437
PRIOR FILING DATE: 2003-07-18
PRIOR FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/396,335
PRIOR APPLICATION NUMBER: US 60/398,617
PRIOR APPLICATION NUMBER: US 60/427,231
PRIOR PLING DATE: 2002-07-26
PRIOR PLING DATE: 2002-11-19
PRIOR PLING DATE: 2003-11-19
PRIOR APPLICATION NUMBER: US 60/456,496
PRIOR PLING DATE: 2003-03-24
PRIOR APPLICATION NUMBER: US 60/474,940
PRIOR APPLICATION NUMBER: US 60/474,940
PRIOR PLING DATE: 2003-06-03
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US-09-896-888A-14
IS-09-896-888A-14

Sequence 14, Application US/09896888A
; Patent No. US20020116723A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: pIB/V5-His-DEST
                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 99.8
Matches 547; Conservative
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240

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300 360 360 420 480 480 540

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09

120 120 180 240

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FEATURE: OTHER INFORMATION: Recombination region of pIB/V5 His DEST
                             PRIOR APPLICATION NUMBER: US 60/396,335
PRIOR FILING DATE: 2002-07-18
PRIOR FILING DATE: 2002-07-18
PRIOR FILING DATE: 2002-07-26
PRIOR FILING DATE: 2002-11-19
PRIOR FILING DATE: 2002-11-19
PRIOR FILING DATE: 2003-13-24
PRIOR APPLICATION NUMBER: US 60/456,496
PRIOR PILING DATE: 2003-03-24
PRIOR PILING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 127
  2003-07-18
NUMBER: US 60/396,335
                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 AGTACAAACTCTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGC 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AGTACAAACTCTACGTTTTCGTAGACTATTTTTACATAAATAGTCTACACCGTTGTATATACGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCAAATACACTACCACATTGAACCTTTTTGCAGTGCAAAAAAGTACGTGTCGGCAGT 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 342 ACGAGTGTTGTCTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGAC 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 ACGAGTGTTGTCTTATCGTGACGCCCAGCTTCCTGTGTTGCTAACCGCAGCCGGAC 300
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APPLICANT: Melch, Peter J.
APPLICANT: Harwood, Steven
APPLICANT: Harwood, Steven
APPLICANT: Frimpong, Kenneth
APPLICANT: Frimpong, Kenneth E.
APPLICANT: Frimpong, Kenneth E.
TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
FILE REFERENCE: 0942.5450007
CURRENT APPLICANTON VURBER: US/10/622,088
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: PCT/US03/22437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence:Promoter; OTHER INFORMATION: sequence of the OpMNPV ie2 gene US-09-896-888A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81.9%; Score 462; DB 9; Length 462; 100.0%; Pred. No. 1.1e-141; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           522 GGTAAACACAGTTGAACAGCATCTGTTACAGCGACACAACAT 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421 GGTAAACACAGTTGAACAGCATCTGTTACAGCGACACAACAT 462
APPLICANT: The University of British Columbia
TITLE OF INVENTION: Insect Expression Vectors
FILE REFERENCE: 80021-44
CURRENT APPLICATION NUMBER: US/09/896,888A
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US/09/048,911
PRIOR APPLICATION NUMBER: 60/049,946
PRIOR PILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/049,946
PRIOR PILING DATE: 1997-03-27
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 127, Application US/10622088; Publication No. US20040219516A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.0
Matches 462; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 7
US-10-622-088-127
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1 CTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAAACACAGTTGAACAGCATCTG 60
                                                                                     0; Gaps
                                                                                                                                                                                                      Length 147;
OTHER INFORMATION: Recombination region of pIB/V5-His-DEST PRATURE:
                                                                                     0; Indels
                                                                  Query Match
11.0%; Score 62; DB 18; 1
Best Local Similarity 100.0%; Pred. No. 8.2e-10;
Matches 62; Conservative 0; Mismatches 0;
                    NAME/KEY: misc_feature

// LOCATION: (141)...(148)

OTHER INFORMATION: n may be any nucleotide

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                                                                                                                                                                                                                                                                                                        487 CTIATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAACACAGTTGAACAGCATCTG 546
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                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                       CTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAAACACACAGTTGAACAGCATCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CTATTTTATTAGAATAGTCTACACTGTACGATACGCTCCCAATATACTACTACTATATCA
                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) OTHER INFORMATION: Description of Artificial Sequence: Fragment of CTHER INFORMATION: promoter sequence of the AcMNPV ien gene US-09-896-888A-16
                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                  11.0%; Score 62; DB 18; Length 325;
100.0%; Pred. No. 1.2e-09;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20; Indels .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 10.1%; Score 57; DB 9; Length 92; Best Local Similarity 77.5%; Pred. No. 2.9e-08; Matches 69; Conservative 0; Mismatches 20; Indels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION: Insect Expression Vectors
FILE REFERENCE: 80021-44
CURRENT APPLICATION NUMBER: US/09/896,888A
CURRENT APPLICATION NUMBER: US/09/048,911
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PRIOR DATE: 1997-03-27
SOFTWARE: PRIOR IN VECTOR OF SEQ ID NOS: 50
SEQ ID NO 16
LENGTH: 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15, Application US/0989688A
Factor No. US20020116723A1
GENERAL INFORMATION
TILLE OF INVENTION: Insect Expression Vectors
FILE REPERSENCE: 80021-44
CURRENT APPLICATION NUMBER: US/09/896, 888A
CURRENT FILING DATE: 2001-06-29
FRIOR APPLICATION NUMBER: US/09/048,911
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16, Application US/09896888A
Patent No. US20020116723A1
                                                        LOCATION: (141)..(142)
OTHER INFORMATION: n is a, c,
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                                                                                                                                                                                                                                       Best Local Similarity 100.
Matches 62; Conservative
FEATURE:
NAME/KEY: misc feature
____TON: (141)..(142)
                                                                                                    ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (145)..(276)
US-10-622-088-149
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TT 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                             75
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                                                                                                                                                                                                                      ) OTHER INFORMATION: Description of Artificial Sequence: Fragment of ; OTHER INFORMATION: promoter sequence of the AcMNPV ien gene US-09-896-888A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Epigenomics AG
TITLE OF INVENTION: Methods and nucleic acids for the analysis of
TITLE OF INVENTION: proliferative disorders
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/473,126
CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-473-126-199
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                                                                                                                                                                                                                                                                                                                             Query Match 7.6%; Score 42.6; DB 9; Length 8 Best Local Similarity 74.0%; Pred. No. 0.0016; Matches 54; Conservative 0; Mismatches 19; Indels
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Publication No. US20040048254A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with
TITLE OF INVENTION: tumor suppressor genes and oncogenes
FILE REFERENCE: 5013.1005
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Pred. No. 0.13;
0; Mismatches 74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 53.2%;
Matches 84; Conservative
                                                                                                                                                                ORGANISM: Artificial Sequence
PRIOR FILING DATE: 1997-03-27
NUMBER OF SEQ ID NOS: 50
SOFFWARE: PatentIn Ver. 2.0
SEQ ID NO 15
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US-10-473-126-199/c
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LENGTH: 628
                                                                                                            LENGTH: 88
                                                                                                                                            TYPE: DNA
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155 CATACATAGTACAAACTCTACGTTTCGTAGACTATTTTACATAAATAGTCTACACGGTTG 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          215 TATACGCTCCAAATACACTACCACATTGAACCTTTTTGCAGTGCAAAAAAGTACG 271
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; Publication No. US20040018514A1
; Publication No. US20040018514A1
; GENERAL INFORMATION:
    APPLICANT: KUNST, Prederik
; APPLICANT: GLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221
CURRENT FILING DATE: 2003-03-27
; PRIOR PLILION DATE: 2003-03-04
; PRIOR FILING DATE: 2000-10-04
; PRIOR FILING DATE: 2000-10-04
; PRIOR FILING DATE: 2000-10-04
; RIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: Patentin Version 3.0
                                                                                                                                                                                 Sequence 1528, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: GLASER, Philippe
; TITLE OP INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221
; CURRENT FILING DATE: 2003-03-27
; PRIOR PLICATION NUMBER: PCT/FR 01/03 061
; PRIOR FILING DATE: 2000-10-04
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: FR 00/12 697
; RAOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARR: PatentIn version 3.0
; SEQ ID NO 1528
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NAME/KEY: misc feature

LOCATION: (1)...(end)

OTHER INFORMATION: n can be any nucleotide: a,g,c or t/u
US-10-398-221-3152
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i OTHER INFORMATION: n can be any nucleotide a,g,c or t/u
US-10-398-221-1528
      4776 ATAGAACTTTCCTCTCTATAAAAACAAAAAAAA 4739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Listeria monocytogenes 4b
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Best Local Similarity
                                                                                                                                         RESULT 14
US-10-398-221-1528/c
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Sequence 345, Application US/10473126

Sequence 345, Application US/10473126

Sequence 345, Application US/10473126

Sequence 345, Application US/10403341

SEQUENCE OF INVERTION:

TITLE OF INVERTION: Methods and nucleic acids for the analysis of hematopoietic cell

TITLE OF INVERTION: proliferative disorders

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/473,126

CURRENT PILING DATE: 2003-09-26

NUMBER OF SEQ ID NOS: 1258

SEQ ID NO 345

LENGTH: 6289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.0%; Score 39.6; DB 17; Length 9289; Best Local Similarity 53.2%; Pred. No. 0.16; Matches 84; Conservative 0; Mismatches 74; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.7%; Score 38; DB 18; Length 6289; Best Local Similarity 52.5%; Pred. No. 0.45; Matches 83; Conservative 0; Mismatches 75; Indels
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CURRENT APPLICATION NUMBER: US/10/221,714A
CURRENT FILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: PCT/EPD1/02955
PRIOR FILING DATE: 2001-03-15
PRIOR PILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: DE 10013047.0
PRIOR PILING DATE: 2000-04-06
PRIOR PILING DATE: 2000-04-06
PRIOR PILING DATE: 2000-04-06
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-09-01
PRIOR PILING DATE: 2000-09-01
PRIOR PILING DATE: 2000-09-01
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Gaps
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Indels
51;
Mismatches
0;
Conservative
99
Matches

155	155 CATACATAGTACAAACTCTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTG 214
881	881 CAGAITIAGAAAACATITAICGIIGCCCAGGAAAAITIAAAIAICAAGAGCACICIGIIG 822

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ò g Search completed: May 10, 2005, 10:28:53 Job time: 1600.6 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Λ \	φ,			28	-10-622-088-12	equence 12
<b>1</b>	4	97.2		27	-10-295-074-6	ednence 60
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ο ,	46			28	-10-622-088-8	e. 89
10	462	81.9	462	16	9-048-911-1	equence 14
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14	62	-	147	28	-10-622-088-12	e 127,
15	62	11.0	325	28	-622-088-14	e 149,
16	57	10.1	92	16	-09-048-911-1	Φ
17	57	10.1	92	38	-09-896-888-1	equence 16,
18	n		92	38	-896-88BA-	equence 16,
19	•	•	88	16	-09-048-911-1	equence
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21	ö	7.6	88	38	-09-896-888A-1	equence
.,	•			22	-10-473-126-19	equence 199,
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.,	6.	٠	9289	20	0-221-714B-2	equence 223,
· ·	38	6.7		55	-10-473-126-34	equence 345.
(A			505	28	-10-664-025-1563	equence
(A	è.	6.5	505	83	-60-147-499-1	equence 15639
c 28	36.2	6.4	425	23	0 - 2521	equence 252142.
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31	m		4	23	-09-521-640-2235	equence 223561
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m ·	'n.		877	20	-10-238-659-	equence 475,
m	'n		σ	23	-10-398-221-152	e 1528,
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m	Ľ.	6.2	36	46	-10-020-338-442	'n
4	35	٠	LO.	21	-10-266-090-352	equence 35243
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4.		•	7		-09-552-087-1117	equence 11171
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ö 120 180 120 180 240 240 300 360 360 420 420 480 480 540 540 9 9 TITICALGITIGCCAACAAGCACCTITATACTCGGTGGCCTCCCCACCACCAACTITITIT GACAGGACGCCAGCTTCCTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACA 1 CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAACTGTG TTTTCATGTTTGCCAACAAGCACCTTTATACTCGGTGGCCTCCCCACCACCAACTTTTTT GTAGACTATTTTACATAATAGTCTACACCGTTGTATACGCTCCAAATACACTACCACAC GGGTCGCGTCCTGTCACGTACGAATCACATTATCGGACCGGACGAGTGTTGTCTTATCGT 301 GGGTCGCGTCCTGTCACGTACGAATCACATTATCGGACCGGACGGGTGTTGTCTTATCGT GACAGGACGCCAGCTTCCTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACA GGACGCCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACACGAGGCGCCC GTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAACACAGTTGAACAG 481 GTCCCGCTTATCGCGCCCTATAAATACAGCCCGCAACGATCTGGTAAACACACAGTTGAACAG CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTG Gaps ö Length 564; Indels ; Score 564; DB 16; ; Pred. No. 5.7e-171; 0; Mismatches 0; US-09-048-911-1

Sequence 1, Application US/09048911

GENERAL INFORMATION:

APPLICANT: The University of British Columbia

TITLE OF INVENTION: Insect Expression Vectors

FILE REPERBENCE: 80021-4

CURRENT APPLICATION NUMBER: US/09/048,911

CURRENT PILING DATE: 1998-03-26

EARLIER FILING DATE: 1997-03-27

NUMBER OF SEQ ID NOS: 50

SEQ ID NO: SEQ ID NO: 2.0

IENGTH: 564 RESULT 2
US-09-896-888-1
Sequence 1, Application US/09896888
GENERAL INFORMATION:
APPLICANT: The University of British Columbia
ITILE OF INVENTION: Insect Expression Vectors
FILE REPERENCE: 80021-44
CURRENT APPLICATION NUMBER: US/09/896,888 541 CATCTGTTACAGCGACACAACATG 564 541 CATCTGTTACAGCGACACAACATG 564 100.0%; , ORGANISM: Orgyia pseudotsugata US-09-048-911-1 Query Match 100. Best Local Similarity 100. Matches 564; Conservative 61 61 121 121 181 241 361 361 421 : DNA 301 421 481 셤 · & g 원 g à ò ò ద à d ò 8 셤 8 g 8 유 ઠ

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; LENGTH: 564
; TYPE: DNA
; ORGAN: SN: Orgyia pseudotsugata
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                                                                                                                                                                                     Length 564;
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                                                                                                                                                                                Query Match 100.0%; Score 564; DB 38; Best Local Similarity 100.0%; Pred. No. 5.7e-171; Matches 564; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: The University of British Columbia TITLE OF INVENTION: Insect Expression Vectors FILE REFERENCE: 80021-4 CURRENT APPLICATION NUMBER: US/09/096, 888A CURRENT FILING DATE: 2001-06-29 FRIOR PLILING DATE: 1998-03-26 FRIOR APPLICATION NUMBER: 60/049,946 FRIOR FILING DATE: 1997-03-77 NUMBER OF SEQ ID NOS: 50 SOFTWARE: Patentin Ver. 2.0
PRIOR APPLICATION NUMBER: US 09/048,911
PRIOR FILING DATE: 1998-03-26
PRIOR APPLICATION NUMBER: US 60/049,946
PRIOR PILING DATE: 1997-03-27
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 1
LENGTH: 564
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                                                                                                                        ; TYPE: DNA
; ORGANISM: Orgyia pseudotsugata
US-09-896-888-1
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US-09-896-888A-1
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                                                              Gaps
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FILE REFERENCE: 0942.545PC7
CURRENT APPLICATION NUMBER: PCT/US03/22437
CURRENT APPLICATION NUMBER: PCT/US03/22437
CURRENT PILLING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 60/396,335
PRIOR APPLICATION NUMBER: US 60/396,617
PRIOR PILLING DATE: 2002-07-26
PRIOR PILLING DATE: 2002-07-26
PRIOR PILLING DATE: 2002-07-26
PRIOR PILLING DATE: 2003-07-26
PRIOR PILLING DATE: 2003-07-26
PRIOR PILLING DATE: 2003-07-26
PRIOR PILLING DATE: 2003-07-26
PRIOR PILLING DATE: 2003-07-24
PRIOR PILLING DATE: 2003-03-24
PRIOR PILLING DATE: 2003-03-24
PRIOR PILLING DATE: 2003-03-24
PRIOR PILLING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 146
SOFTWARE: Patentin version 3.2
SEQ ID NO 126
LENGTH: 560
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        Length 564;
                                                           Indels
  ; Score 564; DB 38;
; Pred. No. 5.7e-171;
0; Mismatches 0;
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     100.0%;
Query Match
Best Local Similarity 100.
Matches 564; Conservative
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                                                                                                            Gaps
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GENERAL INFORMATION:
APPLICANT: Bennett, Robert P.
APPLICANT: Welch, Peter J.
APPLICANT: Harwood, Steven
APPLICANT: Harwood, Steven
APPLICANT: France, Kenneth
TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
FILE REFERENCE: 0942.5450007
CURRENT APPLICATION NUMBER: US/10/622,088
CURRENT APPLICATION NUMBER: ECT/US03/22437
PRIOR PLLING DATE: 2003-07-18
PRIOR PLLING DATE: 2003-07-18
PRIOR PLLING DATE: 2003-07-18
PRIOR PLLING DATE: 2002-07-18
PRIOR PLLING DATE: 2002-07-18
PRIOR PLLING DATE: 2002-07-18
PRIOR FLLING DATE: 2002-11-19
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                                                                                 Length 560
                                                                                                          Indels
                                                                              97.2%; Score 548; DB 2; Le
100.0%; Pred. No. 8.6e-166;
iive 0; Mismatches 0;
                                     OTHER INFORMATION: OPIE2 promoter sequence
                                                                                                          Conservative
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Best Local Similarity
Matches 548; Conserv
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            ORGANISM: Unknown FEATURE:
                                                     PCT-US03-22437-126
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US-10-622-088-126
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US-10-295-074-60
US-10-295-074-60
Sequence 60, Application US/10295074
GENERAL INFORMATION:
APPLICANT: Pharmexa A/S
TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
FILE REPRENCE: PIOLI3DK00
CURRENT APPLICATION NUMBER: US/10/295,074
CURRENT PILING DATE: 2002-11-15
NUMBER OF SEQ ID NOS: 60
SOUTHWARE: Patentin version 3.1
SEQ ID NO 60
LENGTH: 2773
                                                                                                                             ;
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                                                                                                                          0; Indels
                                                                       Query Match 97.2%; Score 548; DB 58; I Best Local Similarity 100.0%; Pred. No. 8.6e-166; Matches 548; Conservative 0; Mismatches 0;
) OTHER INFORMATION: OPIE2 promoter sequence US-10-622-088-126
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420
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       365 GACAGGACGCCAGCTTCCTGTTTGCTAACCGCAGCCGCAACTCCTTATCGGAACA 424
                                                                                                                                                                                      361 GACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACA
                                                                                                301 GGGTCGCGTCCTGTCACGTACGAATCACATTATCGGACCGGACGAGTGTTGTCTTATCGT
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APPLICANT: INFORMATION:
APPLICANT: INFORMATION:
APPLICANT: BARTAT, Tomas
APPLICANT: BARTAT, Tomas
APPLICANT: BARTAT, Tomas
APPLICANT: BARTAT, Tomas
APPLICANT: WOLDBORG, Bjorn
TITLE OF INVENTION: WOVEL IMMUNGENIC MIMETICS OF MULTIMER PROTEINS
FILE REFERENCE: 674542-2018
FILE REFERENCE: 674542-2018
CURRENT APPLICATION NUMBER: US/10/846,911
CURRENT APPLICATION NUMBER: PCT/DK02/00764
PRIOR APPLICATION NUMBER: PCT/DK02/00764
PRIOR FILING DATE: 2002-111-16
PRIOR APPLICATION NUMBER: 60/331,575
PRIOR FILING DATE: 2001-11-16
PRIOR PILING DATE: 2001-11-16
PRIOR PILING DATE: 2001-11-16
SOFTWARE: PatentIN Version 3.1
SEQ ID NO 60
LENGTH: 2773
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US-10-846-911-60
Sequence 60, Application US/10846911; GENERAL INFORMATION:
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LOCATION: (561)...(566)
OTHER INFORMATION: HindIII site
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NAME/KEY: misc recomb
LOCATION: (5737..(578)
OTHER INFORMATION: Aval site
FEATURE:
NAME/KEY: misc recomb
LOCATION: (5867..(591)
OTHER INFORMATION: ECORI site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc recomb
LOCATION: (593). (598)
OTHER INFORMATION: BamHI site
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LOCATION: (625)..(630)
OTHER INFORMATION: ClaI site
FEATURE:
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                                           OTHER INFORMATION: p2ZOp2F expression vector for insect cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 97.2%; Score 548; DB 51; Length 27 Best Local Similarity 100.0%; Pred. No. 1.7e-165; Matches 548; Conservative 0; Mismatches 0; Indels
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NAME/KEY: misc_recomb
LOANING: (2294)..(2299)
OTHER INFORMATION: Aval, Smal, and Xmal site
                                                                                    NAME/KEY: misc recomb
LOCATION: (561)..(566)
OTHER INFORMATION: HindIII site
                                                                                                                                                                                                                                                                          NAME/KEY: misc recomb
LOCATION: (586)..(591)
OTHER INFORMATION: ECORI site
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc recomb
LOCATION: (593)..(598)
OTHER INFORMATION: BamHI site
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LOCATION: (1156)..(1161)
OTHER INFORMATION: ApalI site
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LOCATION: (2551).. (2556)
OTHER INFORMATION: ApaLI site
US-10-295-074-60
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LOCATION: (625)..(630)
OTHER INFORMATION: Clai site
                                                                                                                                                                                 NAME/KEY: misc recomb
LOCATION: (573)..(578)
OTHER INFORMATION: Aval site
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LOCATION: (2204)..(2209)
OTHER INFORMATION: NCOI site
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LOCATION: (629)...(634)
OTHER INFORMATION: ClaI site
FEATURE:
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LOCATION: (2128)..(2133)
OTHER INFORMATION: PetI site
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LOCATION: (2284)..(2289)
OTHER INFORMATION: Aval site
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Best Local Similarity 100.0%; Pred. No. 1.7e-165;
Matches 548; Conservative 0; Mismatches 0;
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NAME/KEY: misc_recomb
LOCATION: (2294)..(2299)
OTHER INFORMATION: Aval, Smal, and Xmal site
                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: misc_recomb
LOCATION: (2551)..(2556)
OTHER INFORMATION: Apall site
US-10-846-911-60
                                                             site
                                                                                                                                                                                    NAME/KEY: misc recomb
LOCATION: (2284). (2289)
OTHER INFORMATION: Aval site
                                                                      FEATURE:
NAME/KEY: misc_recomb
LOCATION: (2128)..(2133)
OTHER INFORMATION: P&LI site
LOCATION: (629)..(634)
OTHER INFORMATION: ClaI site
                                                                                                                       FEATURE:
NAME/KEY: misc recomb
LOCATION: (2204)..(2209)
OTHER INFORMATION: Ncol site
                                 NAME/KEY: misc recomb
LOCATION: (1156)..(1161)
OTHER INFORMATION: Apall
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                                                              TITLE OF INVENTION:

TITLE PEPERENCE: 0942.545FOOT

TITLE REPERENCE: 0942.545FOOT

CURRENT APPLICATION: Viral Vectors Containing Recombination Sites

FILE REPERENCE: 0942.545FOOT

CURRENT APPLICATION NUMBER: PCT/US03/22437

CURRENT FILING DATE: 2003-07-18

PRIOR APPLICATION NUMBER: US 60/396,335

PRIOR PILING DATE: 2002-07-26

PRIOR PLING DATE: 2002-07-26

PRIOR PLING DATE: 2002-07-26

PRIOR PLING DATE: 2003-11-19

PRIOR PLING DATE: 2003-11-19

PRIOR PLING DATE: 2003-04-36

PRIOR PLING DATE: 2003-04-36

PRIOR PLING DATE: 2003-06-03

NUMBER OF SEQ ID NOS: 146

SOFTWARE: PatentIn Version 3.2
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Pred. No. 7.3e-165;
0; Mismatches 1;
PCT-US03-22437-89; Sequence 89, Application PC/TUS0322437; GENERAL INFORMATION:
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COTHER INFORMATION: pIB/V5-His-DEST PCT-US03-22437-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 96.9%;
Best Local Similarity 99.8%;
Matches 547; Conservative C
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61 AGTACAAACTCTACGTTTCGTAGACTATTTTACATAAATAGTCTACACACGTTGTATACGC 120
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US-09-048-911-14

Sequence 14, Application US/09048911

GENERAL INFORMATION:

APPLICANT: The University of British Columbia

TITLE OF INVENTION: Insect Expression Vectors

FILE REPERBENCE: 80021-44

CURRENT APPLICATION NUMBER: US/09/048,911

CURRENT FILING DATE: 1998-03-26

EARLIER FILING DATE: 1997-03-27

NUMBER OF SEQ ID NOS: 50
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US-02-996-888-14
Sequence 14, Application US/09896888
; GENERAL INFORMATION:
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                                                                                              GENERAL INFORMATION;
APPLICANT: Bennett, Robert P.
APPLICANT: Welch, Peter J.
APPLICANT: Welch, Peter J.
APPLICANT: Welch, Peter J.
APPLICANT: Madden, Knut
APPLICANT: Frimpong, Kenneth
APPLICANT: Frimpong, Kenneth E.
TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
FILE REFERENCE: 0942.5450007
CURRENT APPLICATION NUMBER: US/10/622,088
CURRENT PILING DATE: 2003-07-18
PRIOR FILING DATE: 2003-07-18
PRIOR FILING DATE: 2002-07-18
PRIOR PILING DATE: 2002-07-26
PRIOR PELING DATE: 2002-07-26
PRIOR PELING DATE: 2002-07-26
PRIOR FILING DATE: 2002-11-19
PRIOR FILING DATE: 2002-11-19
PRIOR FILING DATE: 2002-11-19
PRIOR FILING DATE: 2003-11-19
PRIOR FILING DATE: 2003-03-24
PRIOR PILING DATE: 2003-03-24
PRIOR PILING DATE: 2003-03-24
PRIOR FILING DATE: 2003-03-34
PRIOR FILING DATE: 2003-03-34
PRIOR FILING DATE: 2003-03-34
PRIOR FILING DATE: 2003-05-33
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PatentIn version 3.2
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Pred. No. 7.3e-165;
0; Mismatches 1;
                                       US-10-622-088-89
; Sequence 89, Application US/10622088
; GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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Best Local Similarity 99.8°
Matches 547; Conservative
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                                                                                                                                                                                                                                                            FEATURE:
CTHER INFORMATION: Description of Artificial Sequence:Promoter
CTHER INFORMATION: sequence of the OpMNPV ie2 gene
US-09-896-888-14
                                                                                                                                                                                                                                                                                                                                                     Length 462;
                                                                                                                                                                                                                                                                                                                                                Query Match 81.9%; Score 462; DB 38; Length 4
Best Local Similarity 100.0%; Pred. No. 5.5e-138;
Matches 462; Conservative 0; Mismatches 0; Indels
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APPLICANT: The University of British Columbia TITLE OF INVENTION: Insect Expression Vectors FILE REFERENCE: 80021-4
CURRENT APPLICATION NUMBER: US/09/896,888
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 69/048,911
PRIOR PILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: US 60/049,946
PRIOR FILING DATE: 1997-03-27
NUMBER OF SEQ ID NOS: 50
SEQ ID NO 14
LENGTH: 462
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82.09-898-888A-14
; Sequence 14, Application US/09896888A
; GENERAL INFORMATION:
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CURRENT FILING DATE: 2003-07-18

PRIOR PRILING DATE: 2003-07-18

PRIOR PILING DATE: 2002-07-26

PRIOR PILING DATE: 2002-07-26

PRIOR PILING DATE: 2002-07-26

PRIOR PILING DATE: 2003-01-19

PRIOR PILING DATE: 2003-03-24

PRIOR PILING DATE: 2003-03-04

PRIOR PILING DATE: 2003-03-05-07

PRIOR PILING DATE: 2003-03-06-03
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0
                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence:Promoter OTHER INFORMATION: sequence of the OpMNFV ie2 gene
                                                                                                                                                                                                                                                                                                                                                                                                    Length 462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Recombination region of pIB/V5-His-DEST FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                   81.9%; Score 462; DB 38; I
100.0%; Pred. No. 5.5e-138;
iive 0; Mismatches 0;
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FT-US03-2437-127
Sequence 127, Application PC/TUS0322437
GENERAL INFORMATION:
TYPE: DNA ORGANISM: Artificial Sequence
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SEQ ID NO 127
LENGTH: 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 462; Conservative
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Best Local Similarity
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Application US/10622088

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                                                                                                                                                                                                                                                                                                                                        487 CTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAACACAGTTGAACAGCATCTG 546
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                                                                                                                                                                                                                                                                   Gaps
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GERREAL INFORMATION:
APPLICANT: Bennett, Reter J.
APPLICANT: Welch, Peter J.
APPLICANT: Welch, Peter J.
APPLICANT: Welch, Peter J.
APPLICANT: Harwood, Steven
APPLICANT: Franke, Kenneth E.
TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
FILE REPERENCE: 0942.5450007
CURRENT APPLICATION NUMBER: 2003-07-18
FILE REPERENCE: 2003-07-18
FRIOR APPLICATION NUMBER: DCT/US03/22437
FRIOR PILING DATE: 2003-07-18
FRIOR PILING DATE: 2003-07-18
FRIOR APPLICATION NUMBER: US 60/396,335
FRIOR PILING DATE: 2002-07-26
FRIOR PILING DATE: 2002-07-26
FRIOR PILING DATE: 2002-11-19
FRIOR PILING DATE: 2002-11-19
FRIOR PILING DATE: 2003-01-16
FRIOR PILING DATE: 2003-01-16
FRIOR PILING DATE: 2003-01-19
FRIOR PILING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 165
FRIOR PILING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 165
FRIOR PILING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 165
FRIOR PILING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 165
FRIOR PILING DATE: 2003-06-03
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                                                                                                                                                                                 Query Match 11.0%; Score 62; DB 2; Length 147; Best Local Similarity 100.0%; Pred. No. 1e-08; Matches 62; Conservative 0; Mismatches 0; Indels
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; NAME/KEY: misc feature
; LOCATION: (141)...(148)
; OTHER INFORMATION: n may be any nucleotide
PCT-US03-22437-127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
| LOCATION: (141)...(148)
| OTHER INFORMATION: n may be any nucleotide
| US-10-622-088-127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 127, Application US/10622088 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 62; Conserva
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RESULT 15 US-10-622-088-149

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| APPLICATY: Bennet, INPORMATION: |
| APPLICATY: Bennet, Robert P. |
| APPLICATY: Bennet, Robert P. |
| APPLICATY: Bennet, Robert P. |
| APPLICATY: Hadden, Kenneth R. |
| APPLICATY: Hadden, Kenneth R. |
| APPLICATY: Franke, Kenneth R. |
| APPLICATION INDER: 000-07-18 |
| PRIOR PRILICA DATE: 2003-07-18 |
| PRIOR PRILICA DATE: 2003-08-14 |
| PRIOR PRILICA DATE: 2003-08-14 |
| PRIOR PRINCA APPLICATION NUMBER: US 60/474,940 |
| PRIOR PRILICA DATE: 2003-08-14 |
| PRIOR PRILICA DATE: 2008-14 |
| PRIOR PRINCA DATE: 2008-14 |
|
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This Pool Bloth Use 101

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Sequence 60, Application US/10939107

GENERAL INFORMATION:
APPLICANT: Pedersen, Hans Rudolf
APPLICANT: Bedresen, Louise Henriette
APPLICANT: Rasmussen, Peter Birk
TITLE OF INVENTION NOVEL APPLICATION NOVEL APPLICANT:
FILE REFERENCE: 674542-2020
CURRENT APPLICATION NUMBER: US/10/939,107
CURRENT APPLICATION NUMBER: PCT/DK03/00147
FILE REPERENCE: 2003-03-11
FRIOR FILING DATE: 2003-03-11
FRIOR FILING DATE: 2003-03-11
FRIOR FILING DATE: 2003-03-11
FRIOR FILING DATE: 2003-03-11
SPRIOR FILING DATE: 2003-03-11
SOFTWARE: PatentIn version 3.1
SOFTWARE: PatentIn version 3.1
SEQ ID NO 60
LENGTH: 2773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: p2ZOp2F expression vector for insect cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: misc recomb
LOCATION: (561)..(566)
OTHER INFORMATION: HindIII site
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OTHER INFORMATION: ECORI site
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NAME/KEY: misc recomb
LOCATION: (573)..(578)
OTHER INFORMATION: Aval site
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OTHER INFORMATION: BamHI
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NAME/KEY: misc recomb
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LOCATION: (625)..(630)
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LOCATION: (593)..(598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -10-939-107-60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 25442, A
Sequence 38495, A
Sequence 38494, A
Sequence 25441, A
Sequence 15168, A
Sequence 15168, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 60, Appl
Sequence 26311, A
Sequence 2178, Ap
Sequence 2179, Ap
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                                                                                                                                  May 10, 2005, 05:51:35; Search time 1390.39 Seconds (without alignments) 834.449 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*

2: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq:*

3: /cgn2_6/ptodata/1/pna/USO6_NEW_COMB.seq:*

4: /cgn2_6/ptodata/1/pna/USO8_NEW_COMB.seq:*

5: /cgn2_6/ptodata/1/pna/USO8_NEW_COMB.seq:*

6: /cgn2_6/ptodata/1/pna/USO9_NEW_COMB.seq:*

7: /cgn2_6/ptodata/1/pna/USO9_NEW_COMB.seq:*

9: /cgn2_6/ptodata/1/pna/USO9_NEW_COMB.seq:*

9: /cgn2_6/ptodata/1/pna/USO9_NEW_COMB.seq:*

10: /cgn2_6/ptodata/1/pna/USO9_NEW_COMB.seq:*

11: /cgn2_6/ptodata/1/pna/USO1_NEW_COMB.seq:*

12: /cgn2_6/ptodata/1/pna/USO1_NEW_COMB.seq:*

12: /cgn2_6/ptodata/1/pna/USO1_NEW_COMB.seq:*

13: /cgn2_6/ptodata/1/pna/USO1_NEW_COMB.seq:*

13: /cgn2_6/ptodata/1/pna/USO1_NEW_COMB.seq:*
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GenCore version 5.1.6
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1 US-11-060-756-2179

1 US-11-060-756-6451

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1 US-11-079-083-1099

1 US-11-079-463-3281

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1 US-11-079-143-38495

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                                                                                                                                                                                                                                                                                                                                                                                                  9398789 seqs, 1028555566 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                        OM nucleic - nucleic search, using sw model
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seq length: 200000000
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Match Length DB
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1391
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Maximum DB
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3563 Sequence 372 Sequence 635 011 Sequence 701	<b>ស ស ស</b>	US60-659-397-12262 Sequence 12262 US-11-031-175-6433 Sequence 6433, US-60-655-875-1528 Sequence 1528, US-11-031-175-1048 Sequence 1048,	42 S 96 386	US-60-669-175-18851 Sequence 18851 S-10-703-032-68319 Sequence 68319, S-10-703-032-53281 Sequence 53281, US-60-655-875-6428 Sequence 6428,	2 8 8 8 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5
US-11-097-143-372 US-60-655-875-635 US-60-655-875-701	US-10-517-441-350 US-10-517-441-624 US-10-450-763-18397	US-60-659 US-11-031 US-60-655 US-11-031	US-11-073-360-16 PCT-US04-31416-50 US-60-660-322-21 US-11-097-143-20	US-60-669-175-1885 US-10-703-032-68319 US-10-703-032-53281 US-60-655-875-6428	US-10-517-441-462 US-10-517-441-736 PCT-USOS-07924-35 US-11-075-185-35 US-11-097-143-25 US-11-031-175-12 PCT-USOS-07924-1
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## ALIGNMENTS

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Sequence 2178, Application US/11060756
GENERAL INFORMATION:
APPLICAMT: Wyeth
APPLICAMT: Wyeth
TITLE OF INVENTION: Target Genes
FILE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-04200))
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Get al.

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DECESCION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DROSOPHILA GENES.
TITLE APPLICATION NUMBER: US/11/097,143
CURRENT PLILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-28
PRIOR PLILING DATE: 1999-110-28
PRIOR PLILING DATE: 1999-110-28
PRIOR PLILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR PLILING DATE: 1999-11-2
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR PLILING DATE: 2000-01-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 ATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FastSEQ for Windows Version 4.0
                                                                                                                                   Sequence 26311, Application US/11097143 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 43008
          545 CATCTGTT 552
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Best Local Similarity
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Best Local Similarity
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CRGANISM: Homo
US-11-060-756-2178
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SEQ ID NO 26311
LENGTH: 18977
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LENGTH: 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAACACAGTTGAACAG 540
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4e-163;
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100.0%; Pred. No. ...
... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_recomb
LOCATION: (2294)..(2299)
OTHER INFORMATION: Aval, Smal, and Xmal site
                                                                                                                                             NAME/KEY: misc_recomb
LOCATION: (1156)..(1161)
OTHER INFORMATION: Apal site
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LOCATION: (2551)..(2556)
OTHER INFORMATION: Apall site
                                                                                                                                                                                                                                                   NAME/KEY: misc recomb
LOCATION: (2128)..(2133)
OTHER INFORMATION: PetI site
                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: misc_recomb
LOCATION: (2284)..(2289)
OTHER INFORMATION: Aval site
                                             NAME/KEY: misc recomb
LOCATION: (629)...(634)
OTHER INFORMATION: ClaI site
                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc recomb
LOCATION: (2204)..(2209)
OTHER INFORMATION: NGOI site
OTHER INFORMATION: ClaI site
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Best Local Similarity 100.
Matches 548; Conservative
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us-09-896-888a-1.rnpn

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TITLE OF INVENTION: Mucleic Acid Arrays for Monitoring Expression Profiles of Drug TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug TITLE OF INVENTION: Target Genes TITLE REFERENCE: AM101083 (301896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SQOTHWARE: Patentin version 3.2
SEQ ID NO 6451
LENGTH: 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Avaion Pharmaceuticals
TITLE OF INVENTION: Determining Cancer-Linked Genes and Therapeutic Targets Using
TITLE OF INVENTION: Molecular Cytogenetic Methods
TITLE OF INVENTION: Molecular Cytogenetic Methods
FILE REFERENCE: 689290-237
CURRENT APPLICATION NUMBER: PCT/USO5/07748
CURRENT FILING DATE: 2005-03-08
PRIOR FILING DATE: 2005-03-08
NUMBER OF SEQ ID NOS: 3049
SOFTWARE: Patentin version 3.3
SEQ ID NO 6
LENGTH: 3057
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                                                                  469 AAATAATGITTGGTGGAAATGITCATTAAACATCATTACAAATTTAATGAAAAAGCATGC 410
                                                                                                               70 TIGCCAACAAGAACCTITATACTCGGTGGCCTCCCCACCACCAACTITITIGCACTGCAA 129
                                                                                                                                                        409 ATTTGTACAAGATAGGATACCCCAGGTATATTCAGTCCCATGATTTTTTTGAATGTCAT 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  469 AAATAATGITTGGTGGAAATGTTCATTAAACATCATTACAAATTTAATGAAAAAGCATGC 410
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                       69
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                          10 AAACAATGTATGGTGCTAAATGTTGCTTCAACAACAATTCTGTTGAACTGTGTTTTCATGT
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Pred. No. 1.5;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                              Sequence 6451, Application US/11060756 GENERAL INFORMATION:
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PCT-US05-07748-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.0%;
Best Local Similarity 54.4%;
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
CORGANISM: Homo sapiens
US-11-060-756-6451
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ORGANISM: Artificial
FEATURE:
                                                                                                                                                                                                                                                     349 CTAAA 345
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PCT-US05-07748-6/c
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TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
TITLE OF INVENTION: Target Genes
FILE REFERENCE: AM101083 (031896-042000)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: Patentin version 3.2
SEQ ID NO 2179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug TITLE OF INVENTION: Target Genes PILE REPERENCE: AM101083 (031896-04200)
CURRENT APPLICATION NUMBER: US/11/060,756
CURRENT FILING DATE: 2005-02-18
NUMBER OF SEQ ID NOS: 303284
SOFTWARE: PatentIn version 3.2
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                                                                       469 AAATAATGTTTGGGGAAATGTTCATTAAACATCATTACAAATTTAATGAAAAAGCATGC 410
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                                               10 AAACAATGTATGGTGCTAATGTTGCTTCAACAACTATTCTGTTGAACTGTGTTTTCATGT
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  57; Indels
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54.4%; Pred. No. 1.5;
tive 0; Mismatches 57;
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0; Mismatches
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US-11-060-756-6450/c
Sequence 6450, Application US/11060756
GENERAL INFORMATION:
APPLICANT: Wyeth
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; GENERAL INFORMATION:
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Best Local Similarity 54.4%;
Matches 68; Conservative
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Best Local Similarity 54.4
Matches 68; Conservative
68; Conservative
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COGANISM: Homo sapiens
US-11-060-756-2179
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ORGANISM: Homo sapiens
US-11-060-756-6450
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US-11-060-756-2179/c
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                     57; Indels
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IITLE OF INVENTION: METHODS FOR GENETIC CONTROL OF HETE
IITLE OF INVENTION: IN PLANTS AND COMPOSITIONS THEREOF
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 54.4%; Pred. No. 2.6;
tive 0; Mismatches
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6.0%; Score 33.6; Di
Best Local Similarity 66.7%; Pred. No. 2.3;
Matches 48; Conservative 0; Mismatches
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CURRENT FILING DATE: 2005-02-24
NUMBER OF SEQ ID NOS: 171306
                                                                                                                                                                                                                                                                                                        Sequence 26427, Application US/60655875
GENERAL INFORMATION:
APPLICANT: Boukharov, Andrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
; LOCATION: (1380)..(1381)
; OTHER INFORMATION: n is a, c, g, or t
US-60-655-875-26427
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Miller, Nancy
Williams, Deryck
Vaudin, Mark
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Guo, Liang
Kovalic, David
Lu, Maolong
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LOCATION: (1051)..(1051)
OTHER INFORMATION: n is a,
                   68; Conservative
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Best Local Similarity
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US-10-472-963-1098
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APPLICANT:
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Sequence 1098, Application US/10472963
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVERTION: Human Secreted Proteins
FILE REFERENCE: PS954PCT
CURRENT APPLICATION NUMBER: US/10/472,963
CURRENT FILING DATE: 2003-09-25
PRIOR APPLICATION NUMBER: PCT/US02/09370

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APPLICANT: GALY L. Breton
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO BACTEROIDES FRA
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22475 CAACAACTCTTCTGTTCCATTGGGACTTTCAGTTCGTGAACCTCACCTTTTACAGTCTGT 22534
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TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION: Human Secreted Proteins
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/472,963
CURRENT FILING DATE: 2003-09-25
FRIOR APPLICATION NUMBER: PCT/US02/09370
FRIOR FILING DATE: 2002-03-26
FRIOR APPLICATION NUMBER: US 60/278,650
FRIOR FILING DATE: 2001-03-27
FRIOR FILING DATE: 2001-09-12
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PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/278,650
PRIOR FILING DATE: 2001-03-27
PRIOR PELING DATE: 2001-09-12
PRIOR FILING DATE: 2001-09-12
PRIOR FILING DATE: 2001-09-12
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 1834
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1098
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Best Local Similarity 56.4%;
Matches 62; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 5.9%;
Best Local Similarity 56.4%;
Matches 62; Conservative
                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-472-963-1098
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US-10-472-963-1097
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US-10-472-963-1097
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US-11-079-463-3281
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US-11-U9/143-1495, Application US/11097143

Sequence 38495, Application US/11097143

GENERAL INFORMATION:
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DROSOPHILA GENES.
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
PRIOR PELING DATE: 1999-10-19
PRIOR PELING DATE: 1999-11-12
PRIOR PELING DATE: 2000-01-12
PRIOR PELING DATE: 2000-03-24
PRIOR PELING DATE: 2000-03-24
PRIOR PELING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FRASERQ for Windows Version 4.0
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                                                                     PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-11-12
PRIOR PLING DATE: 1999-11-12
PRIOR PLING DATE: 1999-12-28
PRIOR PLING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-12-28
PRIOR PLING DATE: 2000-01-12
PRIOR PLING DATE: 2000-01-12
PRIOR FILING DATE: 2000-03-23
PRIOR FILING DATE: 2000-03-23
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: PESESEQ for Windows Version 4.0
SERIOTH: 1268
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Seguence 3281.
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Secuence 3281.
Seguence 3281.
Seguence 3281.
Seguences Relating TO BACTEROIDES FRA TITLE OF INVENTION: WOUNDER: US/11/079,045
FILE REFERENCE: PATHOO-03DIV1
CURRENT APPLICATION NUMBER: US/11/079,045
CURRENT FILING DATE: 2005-031-4
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 1999-04-09
PRIOR FILING DATE: 2000-04-04
NUMBER: US 09/540,209
PRIOR FILING DATE: 2000-04-04
NUMBER: OF SEQ ID NOS: 10444
SEQ ID NOS: 10444
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GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CLOODAR CONTENT APPLICATION NUMBER: US/11/097,143
CURRENT APPLICATION NUMBER: US/11/097,143
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0; Mismatches
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Pred. No. 5.3;
0; Mismatches
; FILE REFERENCE: PATH00-03DIV2; CURRENT APPLICATION NUMBER: US/11/079,463; CURRENT FILING DATE: 2005-03-14
PRIOR APPLICATION NUMBER: US 60/128,705; PRIOR FILING DATE: 1999-04-09; PRIOR FILING DATE: 1999-04-09; PRIOR PILING DATE: 2000-04-04; NUMBER OF SEQ ID NOS: 10444; SCQ ID NOS: 10444; SCQ ID NOS: 1221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 32.4;
Pred. No. 5.
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Best Local Similarity 55.39
Warches 63; Conservative
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Best Local Similarity 55.3
Matches 63; Conservative
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US-11-079-045-3281
                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: B.fragilis
US-11-079-463-3281
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APPLICANT: Venter, J. Craig
APPLICANT: et al.

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DROSOPHILA GENES.

TITLE OF INVENTION NUMBER: 00/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR FILING DATE: 1999-10-05
PRIOR PELICATION NUMBER: 60/157,832
PRIOR PELICATION NUMBER: 60/160,191
PRIOR PELICATION NUMBER: 60/160,191
PRIOR PELING DATE: 1999-11-12
PRIOR PELING DATE: 1999-11-12
PRIOR PELING DATE: 1999-11-12
PRIOR PELING DATE: 1999-11-12
PRIOR PELING DATE: 1999-11-228
PRIOR PELING DATE: 1999-11-228
PRIOR PELING DATE: 1999-11-228
PRIOR PELING DATE: 2000-01-12
PRIOR PELING DATE: 2000-01-24
PRIOR PELING DATE: 2000-01-24
PRIOR APPLICATION NUMBER: 60/173,831
PRIOR PELING DATE: 2000-01-24
PRIOR PELING DATE: 2000-01-33
PRIOR PELING DATE: 2000-01-32
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Pred. No. 5.5;
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US-11-097-143-38494/c
; Sequence 38494, Application US/11097143
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 51.4%;
Matches 75; Conservative (
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Best Local Similarity 51.4%;
Matches 75; Conservative (
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; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-38495
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Search completed: May 10, 2005, 09:51:25 Job time : 1391.39 secs

15.6   6.3   665   9   CL742215   CL742215   OR_BBB007     35.6   6.3   787   8   AQ857977   AL18886   Tetracdon     35.4   6.3   755   AQ751255   AQ751255   HS ETROCON     35.4   6.3   755   AQ751255   CC706618   EFIO. Pē0     35.4   6.3   957   9   CG020891   CG020891   EFIO. Pē0     35.5   6.2   1019   9   CG620891   CC661440   DEC6055     35.5   6.2   1019   9   CMS 00LO     35.5   6.2   1019   9   CMS 00LO     35.6   6.2   1019   CMS 00LO     36.7   7   7   7   7   7     37.8   6.2   98   9   CMS 0067B   CC6080859   AGENCOURT     34.8   6.2   711   7   CM7 55468   CC6080859   AGENCOURT     34.8   6.2   217   9   CMS 00167B   CC6080859   AGENCOURT     34.8   6.2   217   9   CL645025   CL645025   CL645025     34.6   6.1   172   9   CMS 0017GN   CL65080   CC675017   C197-3681     34.6   6.1   1123   9   CMS 0017GN   CC675017   C197-3681     34.4   6.1   249   CG57807   CG57807   CG57807     35.6   CMS 001807   CG57807   CG57807     36.7   CMS 001807   CG57807   CG57807     37.7   CMS 001807   CG57807   CG57807   CG57807     37.7   CMS 001807   CG57807   CG57807   CG57807     37.7   CMS 001807   CG57807   CG57807   CG57807   CG57807   CG57807   CG57807   CG57807   CG		Bombyx mori cDNA Unpublished (2000) Contact: Mita K Genome Research Group National Institute of Agrobiological Sciences Owashi 1-2, TBukuba, 1Baraki 305-8634, Japan Bamail: Kumita@mias.affrc.go.jp method:uni-directional, Sequence direction:sequenced Email: TBukuba, 1Baraki 305-8634, Japan Email: Mita@mias.affrc.go.jp method:uni-directional, Sequence direction:sequenced project=-Silkworm Genome Program in MAFF, and Resea Future Program in JSPS' see 'SilkBase', chttp://www.ab.a.u-tokyo.ac.jp/silkbase', for whole Location/Qualifiers in . 679  / Corganism=-Bombyx mori" / Mol_type="RRNA" / Mol_type="RRNA" / Mol_type="RNNA" / Ab xref="Taxon:7091" / Clone="NV060140" / Lisue type="Dam cultured cell" / Clone="NV060140" / Lisue type="Dam cultured cell" / Clone="Lb="Bombyx mori ovary BmNPV infected incoulation" / Clone lib="Bombyx mori ovary BmNPV infected incoulation" / Clone lib="Bay contacted by incoulation" / Clone lib="Bay contacted by incoulation" / Clone lib="Bay contacted by incoulation" / AbaaAacacaccaracaracaracaracaracaracaracar
0 0 00 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 AV39860 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	FEATURES SOURCE SOURCE SOURCE SOURCE MATCHES MATCHES Db
5.1.6 Compugen Ltd. ch time 3951.56 Seconds ithout alignments) 132.847 Million cell updates/sectgttacagcgacacaacatg 564 saidues sters: 68479088		Description Description Description Description A039860 AC075412 PBH517933 BC0751412 PBH517933 BC0751412 PBH517933 BC0751412 PBH517933 BC0751412 PBH517474 BC0384338 AA137474 BE1843287 FCC9384338 AA137474 BE1843287 FCC9384318 AA137474 BE1843287 FCC9385894 MBG695019 MBG695019 BE374425 6C2510716 SBM278655 AC7753134 OAG401197 MBG695519 MBG695019 MBG695019 MBG695019 MBG695019 MBG695019 MBG6951197 MBG697 M
GenCore version 5.1.6  Copyright (c) 1993 - 2005 Compugen  OM nucleic - nucleic search, using sw model  Run on:  May 10, 2005, 03:45:00; Search time (without a 5432.847 M  Title: Perfect score: 564 Sequence: Scoring table: IDENTITY NUC Gapop 10.0, Gapext 1.0  Searched: 34239544 seqs, 19032134700 residues  Total number of hits satisfying chosen parameters:	seq length: 0 seq length: 20000 sing: Minimum Mat Maximum Mat Listing fil EST:* 1: 9D-est: 2: 9D-est: 3: 9D-htc: 4: 9D-est: 5: 9D-est: 6: 9D-est: 7: 9D-est: 7: 9D-est: 9: 9D-gss: 8: 9D-gss: 9: 9D-gss: 9: 9D-gss: 0: 1s the numbé	Core derived by a second is derived by a second by a s

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REFERENCE AUTHORS

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Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 109J14. 109J14 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene. Further details:
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Pristionchus pacificus
Bukaryota, Metazoa, Nematoda, Chromadorea, Diplogasterida,
Bukaryota, Metazoa, Nematoda, Chromadorea, Diplogasterida,
Bukaryota, Nematoda, Pristionchus,
1 (bases 1 to 1324)
Srinhivasan,J., Sinz,W., Jesse,T., Wiggers-Perebolte,L., Jansen,K.,
Buntiavasan,J., yan der Meulen,M. and Sommer,R.J.
An integrated physical and genetic map of the nematode Pristionchus
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
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Max-Planck-Institute for Developmental Biology
Spenannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                       http://www.sanger.ac.uk/Projects/D_rerio/
   Location/Qualifiers
                                                                                                                                                                       1 (bases 1 to 762)
Humphray, S.J., Huckle, E. and Durham, J.L.
Direct Submission
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Pred. No. 0.71;
0; Mismatches
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/organism="Danio
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  BX147578.1 GI:27978953
                                                Danio rerio (zebrafish)
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Best Local Similarity 56.7%;
Matches 72; Conservative C
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CH216-145B11 Sp6.1 CH216 Xenopus tropicalis genomic clone
CH216-145B11, genomic survey sequence.
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Renopus tropicalis

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Renopodinae; Xenopus; Silurana.

(bases 1 to 954)

Kremitzki, C., Carter, J., McPherson, J., Warren, W., Graves, T.,

A physical map of the xenopus tropicalis genome

Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="male"
/cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH316"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC_library"
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BX147578
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Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seg primer: Sp6 ATTTAGGTGACACTATAG
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/strain="Nigerian frog"
/db_xref="taxon:8364"
/clone="CH216-145B11"
                                                                                                                                                121 TTTTTGATTACAAAAAGTTCATTTTTGC 150
                                                                                                                    249 TTTTTGCAGTGCAAAAAAGTACGTGTCGGC
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High quality sequence stop: 226.
Location/Qualifiers
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Matches 87; Conserv
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Email: est@watson.wustl.edu
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Matches 97; Conservative
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BOGBL87TF BOGB Brassica oleracea genomic clone BOGBL87, genomic
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Mukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
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                                                             /db_xref="taxon:54126"
/clone lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest
/note="The Dibrary was generated by a partial digest
vector."
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Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea (Unpublished (2001)
Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1272 regaaaaaaacarrrrrccacccccararrrrrrrcccaaaagr 1322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    218 ACGCTCCAAATACACTACCACATTGAACCTTTTTGCAGTGCAAAAAGT 268
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: FF
Sed brases ends.
                                                                                                                                                                                      DB 9; Length 1324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9712 Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                          AACAACAATTCTGTTGAACTGTGTTTTCATGTTTGCCAACAAGCACCTT
                                                                                                                                                                                      Score 39; DB 9; Length 132
Pred. No. 0.81;
0; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79; Indels
         /organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strāin="California"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Brassica oleracea"
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/strain="TO1000DH3"
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/note="Vector: pHOS1;
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/clone="BOGBL87"
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                                                                                                                                                                                       Query Match 6.9%;
Best Local Similarity 48.1%;
Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86; Conservative
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Best Local Similarity
Matches 86; Conserva
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                                                    468
                                                                                                                                                                     Mammalia; Butheria; Primates; Catarrhin; Hominidae; Homo.

(bases 1 to 535)
Hiller, L. Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,
Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N.,
Raddis, E., Moore, B., Mortle, M., Parsons, J., Prange, C., RiKin, L.,
Rohliing, T., Schellenberg, K., Soares, M. B., Tan, F., Thierry-Meg, J.,
Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This clone is available royalty-free through LLNL , contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: ml3 -40 forward High quality sequence stop: 246.
                                                       527 CCAGTTGGTTTGCACTTTACAAGATTAATGATCAGTACTCTCATCAACAAATATTATAAA
                                                                                                                 170 CTCTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of Medicine
4444 Forcest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                       N63392 . 535 bp mRNA linear EST
7235h10.s1 Morton Fetal Cochlea Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue type="cochlea"
/dev_stage="16-22 week fetus"
/lab_host="SOLR cells (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.8%; Score 38.2; DB 7; Length 535;
49.2%; Pred. No. 1.2;
tive 0; Mismatches 100; Indels (
                                                                                                                                                                                                                               230 CACTACCACACTTGAACCTTTTTGCAGTGCAAAAAGTACGTGT 274
                                                                                                                                                                                                                                                                                          407 AAATTCAATACAATTAAATATGTAAAAAATAAAAATATAGACATTT 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Homo sapiens"
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/db_xref="GDB:3892208"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .MAGE:285091 3', mRNA sequence.
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/clone="IMAGE:285091"
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BZ902838/c DEFINITION ACCESSION VERSION

KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

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Department of Animal Sciences
University of Illinois at Urbana Champaign
University of Illinois at Urbana, IL 61801, USA
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewinomiuc.edu
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering_information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by by University of Illinois at Urbana
Champaign, USA with funds provided by grant No. AG202-34480-11828
from USDA-CSRESS and Ag699-35205-8534 from USDA/NRI (Livestock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOTAING, DOTAIN TO SER TO SER TO SERVING, A., Rebeiz, M., Schweitzer, P., Larkin, D.M., Everts-van der Wind, A., Rebeiz, M., Schweitzer, P., Bachman, S., Green, S., Campos, E.J., Benson, L.D., Edwards, J., Liu, L., Womack, J.E., de Jong, P.J. and Lewin, H.A.
A Cattle-Human Comparative Map Built with Cattle BAC-ends and Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BZ899636 582 12-JUN-2003 CH240 16P5.TV CHORI-240 Bos taurus genomic clone CH240_16P5, genomic survey sequence.
                                                                                                                                                   193
                                                                                                                                                                                                               61 TITICATGITIGCCAACAAGCACCTITAIACICGGIGGCCTCCCCACCACCAACTITITI 120
                                                                                                                                                                                                                                                                     192 TTTACCAAGCTTTTAAACACCACATTTATGTTTTTGGGCCTAAATCATCAGCAAATGAATT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cell_type="Blood"
/clone_lib="CHOR1-240"
/note="Vector: pTARBAC1.3; Site_1: Mbol; Site_2: Mbol;
Hereford bull 11 Domino 99375; CHOR1-240 Bovine BAC
library (Male) produced by Pieter de Jong"
                                                                                                                                                   252 CATGCTGATCAATGAGGCATAAAGATATAATTGGTTATAGACACATTTGTTGGAATGTA
                                                                                             1 CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTG
                                       Gaps
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                                    Indels
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         Similarity 55.2%; Pred. No. 1.4; 74; Conservative 0; Mismatches
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Pred. No. 1.4;
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/strain="breed: Hereford"
/db_xref="taxon:9913"
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Plate: 16 row: P column: 5
Seq primer: T7
Class: BAC ends.
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Contact: Harris Lewin
                                                                                                                                                                                                                                                                                                                                                                                       132 TCAGCATTAAAAA 119
                                                                                                                                                                                                                                                                                                                              121 GCACTGCAAAAAA 134
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         Best Local Similarity
Matches 74; Conserv
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Best Local Similarity
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BZ899636
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Genomic Survey sequence.
BZ902838.1 GI:31627927
GSS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Larkin,D.M., Everts-van der Wind,A., Rebeiz,M., Schweitzer,P., Bachman,S., Green,S., Campos,E.J., Benson,L.D., Edwards,J., Liu,L., Wonmack,J.E., de Jong,P.J. and Lewin,H. A. Cattle BAC-ends and Human A Cattle-Human Comparative Map Built with Cattle BAC-ends and Human
                                                                                             275
218 ATGTATACCTCTAACAGTTAGCTTGTAAAAAAAAAACAAAAAAGAAAAAACCATTTT 277
                                                                                                                                                                                                            276 GGCAGTCACGTAGGCCGGCCTTATCGGGTCGCGTCCTGTCACGTACGAATCACATTATCG 335
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Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                          ATACGCTCCAAATACACTACCACACTTGAACCTTTTTGCAGTGCAAAAAAGTACGTGTC
                                                                                                                                                278 ATTTGCCCAAATTTCACCAGGTTTTACTTAAAAATTCTACCTTATGGGTAAATACCAGGC
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Hereford bull_Li Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"
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Unpublished (2003)
Other GSSs: CH240_23B3.TV
Contact: Harris Lewin
Department of Animal Sciences
University of Illinois at Urbana Champaign
1201 W. Gregory Dr., Urbana, IL 61801, USA
Tel: 217_333_598
Fax: 217_244_5617
Email: h-lewin@ulic.edu
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/clone="CH240_23B3"
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1 (bases 1 to 578)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: SP6
Class: BAC ends
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Query Match

ORIGIN

source

FEATURES

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/tissue type="dorsal blastopore lip"
/lab_host="Top10"
/lab_host="Top10"
/lab_host="Top10"
/clone lib="Blumberg Cho dorsal blastopore lip"
/clone lib="Blumberg Cho dorsal blastopore lip"
/note="Organ: embryo; Vector: pBluescript SK-; Site_l:
BCORI; Site=2: Xhol; Library was prepared from 50 ug of
transcriptase. After addition of EcoRI linkers and
ECORI-Xhol digestion, the cDNA was size selected by
chromatography on Sepharose CL-4B columns and fractions
containing cDNAs larger than 500 bp waere ligated into
ECORI-Xhol-digested lambda ZAPII (UniZAP-XR) and packaged
in vitro. Average insert size is 1.4 kb. The original
library contained 6 x 106 recombinants, of which 3 x 106
were amplified and stored at -7.0 C in SM buffer containing
7% DMSO. 3 x 106 pfu were mass excised and the resulting
phagemids used to infect Top10F. References: Science 253,
196-196 and Mathods in Molecular Blology 97, S55-574.
Additional sequences from this library have been deposited
under the name Xenopus laevis dorsal blastopore lip.
Library constructed by Bruce Blumberg (University of file of the page of the
                                                                                                                                                                                                                                                                                            EST 30-JUN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Daniela S. Gerhard, Ph.D.
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rml0A07 Betheada, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Bruce Blumberg
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://inage.llnl.gov
   126 TTTTTGATGCAATATATTTGCCAAAAAACTCAGCTTTTATTTTCCATTTTAAACAACTA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 669)
NIH-MC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                         CO384338 669 bp mRNA linear EST 30-JUN
AGENCOURT_26189343 Blumberg_Cho dorsal blastopore lip Xenopus
Laevis CDNA clone IMAGE:7297357 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone="IMAGE:7297357"
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High quality sequence stop: 5
Location/Qualifiers
                                                                                                                           186 caararrracaagcigir 203
                                                                                                                                                                                                                                                                                                                                                                                                                        CO384338.1 GI:49490161
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                                                                  235 CCACACATTGAACCTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sex="both"
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Best Local Similarity 57.93
Matches 66; Conservative
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AUTHORS
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CO384338
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KEYWORDS
SOURCE
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DNA Sequencing Dy: National Institutes of Health Intramural
Sequencing Center (NISC)
Sequencing Center (NISC)
Clone distribution: NGI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
infochange.llnl.gov
Plate: LLAM12849 row
Seq primer: -21M13 forward primer (ABI).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CB410241 425 bp mRNÀ linear EST 24-MAR-2003
NISC_nc10d09.x1 COGENE 6E MAX Homo sapiens cDNA clone IMAGE:5776553
3', mRNA sequence.
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//olone lib="COENE 6E MAX"
//olone="Vector: pAMP1; cDNA primed using oligo-dT primer,
directionally cloned into UnG sites of pAMP1. Size
selected for insert sizes ranging from 0.2-18 kb.
Normalized to Cot5. Primary library, non-amplified.
Library constructed by M. Lovett. For more information on
Library, please contact R. Tidwell (Washington
University) or visit the COGENE website at
http://hg.wustl.edu/COGENE/."
                                                                                                                                                                                           TITICATGITIGCCAACAAGCACCITTATACTCGGTGGCCTCCCCACCACCAACTTTTT 120
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                                                                                                              265 CATGCTGATCAATGAGCATAAAGATATAATTGGTTTAATGACACATTTGTTGGAATGTA 324
                                                                                                                                                                                                                                                       .325 ritraccaagcitttaaacaccacaritrargtrittgggccraaarcarcagcaaargaarr 384
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 425)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
                                                               1 CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTG
   Gaps
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   60; Indels
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/dev_stage="6 weeks postconception"
/lab_host="DH10B"
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov cDNA Library Preparation:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="1MAGE:5776553"
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                                                                                                                                                                                                                                                                                                                          121 GCACTGCAAAAAA 134
                                                                                                                                                                                                                                                                                                                                                                                   385 TCAGCATTAAAAA 398
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74; Conservative
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Matches 75, Conserv
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6.5%; Score 36.6; DE 50.9%; Pred. No. 3.7; tive 0; Mismatches
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                                                                                                                                                    Danio rerio (zebrafish)
                                                                                                    AI437474.1 GI:4286113
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Best Local Similarity 50.99
Matches 87; Conservative
                                                                                                                                                                          Danio rerio
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                              DEFINITION
                                                                                                                                                                          ORGANISM
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JOURNAL
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                                                                                               VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web: www.genoscope.cns.fr.

Web: www.genoscope.cns.fr.

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcokI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pland BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                1101 bp DNA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence T7 end of BAC # BACK8012 of RPCI-98 library from Drosophila melanogaster (fruit AL063938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    949
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CCCATACATAGTACAAACTCTACGTTTCGTAGACTATTTTACATAAATAGTCTACACGT 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1008 CMCACYYAYWCACAAMCCMTCCCTCTTATAATAACATCTAATAATCAWMAAYTACMAH
                                             104 CCAATAAATAGGGGAACCTTCTGGTATAGTTGTAAAGAATACATCCAATGTATGCAACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133 AACACGCTTTTGCACGCGGGCCCATACATACAAACTCTACGTTTCGTAGACTATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
I (bases 1 to 1101)
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                                                                                            213 TGTATACGCTCCAAATACACTACCACATTGAACCTTTTTGCAGTGCAAAAAA 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        th 6.5%; Score 36.8; Di Similarity 35.9%; Pred. No. 3.9; 61; Conservative 35; Mismatches
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Drosophila melanogaster
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/clone="BACR08012"
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/note="end : T7"
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Best Local S:
Matches 61
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                                                                                                                                                                                                                RESULT 11
CNS0039X/c
                                                                                                                                                                                                                                                               LOCUS
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TITLE
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Genome Systems, St. Louis, Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) (email contact: www.resgen.com) (email contact: address: www.resgen.com) (email contact: address: www.resgen.com) and RescourcenZentrumPrimarDatenbank, Berlin, Germany (web address: www.rspg.de)
                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                       Lark, M., Johnson, S. L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Washu Zebrafish EST Project 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1998)
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forset Park Parkway, Box 8501, St. Louis, MO 63108, USA
Fel: 314 286 1810
A1437474 432 bp mRNA linear EST 07-:
EB34b06.x1 Zebrafish WashU MPIMG EST Danio rerio cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: zbrafish@watson.wustl.edu
                                                            IMAGE:3713747 3', mRNA sequence.
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/sex="mixed"
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/db xref="taxon:7955"
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RESULT 12 AI437474

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DB 1; Length 432; 84; Indels ö

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HTC 19-AUG-2004

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DEFINITION

RESULT 13

BI843287

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE

AUTHORS

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CB484581 GI:29295807

CE484581.1 GI:29295807
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                                                                       82 ACCTITATACTCGGTGGCCTCCCCACCACCACTTTTTTGCACTGCAAAAAAACACGCTT 141
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Submitted (10-AUG-2004) Genoscope - Centre National de Sequencage
Submitted (10-AUG-2004) Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
(E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
More information available at
http://www.genoscope.cns.fr/tetraodon.
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                                                                                                                                                                                                                       169 ACTCTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAAŢ
                                                                                                                                                                                                                                                                                    87 AGTGAACAATTTACAAATATATAAAACAACAACTGTTTTCTGTTGGCTACTAAGCACTT
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                                                                                                                                                                                                                                                                                                                                                                    229 ACACTACCACACTTGAACCTTTTTGCAGTGCAAAAAAGTACGTGGCGCA 279
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   Indels
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Tetraodon nigroviridis
Tetraodon nigroviridis
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   84;
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Pred. No. 4.5;
0; Mismatches 95;
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       Mismatches
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/db_xref="taxon:99883"
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Best Local Similarity 49.5%;
Matches 93; Conservative
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       87;
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ACCESSION
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CR709617/c
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/lab host="DH10B (phage-resistant)"
/lab host="DH10B (phage-resistant)"
/clone_lib="Gong zebrafish voary"
/note="Organ: ovary (pooled); Vector: pBluescript SK-;
Site_1: Xho1; Site_2: EcoRI; Poly A+ RNA was isolatd from
the ovaries of 2 female adult zebrafish (4-5 month old).
cDNAs were made using oligo-dT primers and inserted into
lambda ZAP II vector (Stratagene) by Dr. Z. Gong, in vivo
mass-excised to pBluescript SK- following the Washington
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                                                                                                             ACTCTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAAT 228
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1 (Bases 1 to 580)
1 (Bases 1 to 580)
2 (lark,M., Johnson,S.L., Lehrach,H., Lee,R., Lii,F., Marra,M., Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,B., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., WashU Zebrafish EST Project 1998
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Please contact Zhiyuan Gong for further information on
this library (National University of Singapore,
Department of Biological Sciences, Lower Kent Ridge Road,
Singapore 119260)."
The library was constructed by Dr. 2. Gong. DNA Sequencing by:
Washington University Genome Sequencing Center St. Louis. Please
contact Zhiyana Gong for further information on this library
(National University of Singapore, Department of Biological
Sciences, Lower Kent Ridge Road, Singapore 119260).
                                                                                                                                                                                  AGTGAACAATTTACAAATATATAAAACAACAACTGTTTTCTTTGCTTACTAAGCACTT
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                             ACACTACCACATTGAACCTTTTTGCAGTGCAAAAAGTACGTGTCGGCA 279
                                                                                                                                                                                                                                                                                                           141 ACTCTACTACACACTTCAATTACACGGAGAGCCTAAAAGTACATGACAGAA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BI843287
ft59f05.xl Gong zebrafish ovary Danio rerio cDNA clone
IMAGE:5157656 3', mRNA sequence.
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Pred. No. 3.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: zbrafish@watson.wustl.edu
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/mol_type="mRNA"
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Location/Qualifiers
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Fax: 314 286 1810
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Best Local Similarity
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Gaps

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FEATURES

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                                                Coregonic Cupeaformis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Coregonus.

(Dases 1 to 480)

GRASP Consortium, Davidson, W.S., Koop, B.F. and
http://web.uvic.ca/cbr/grasp.

A Burvey of Salmo salar transcripts from high complexity cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: bkoop@uvic.ca
Centre for Biomedical Research, University of Victoria cDNA
preparation and sequencing: Roberto Alberto, Marianne
Beetz-Sargent, Maura Busby, Peter Hunt, Linda McKinnel, BF Koop.
bioinformatics: Gordon D Brown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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                                                                                                                                                                                                                                                                                                                         Contact: Koop BF (
Centre for Blomedical Research
University of Victoria
PO Box 3020 STN CSC, Victoria BC, V8W 3N5, Canada
Fat: 250 472 4057
Fat: 250 472 4075
Email: bkoop@uvic.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Coregonus clupeaformis"
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                               Coregonus clupeaformis
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Unpublished (2002)
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AUTHORS
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